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                        GenCore version 5.1.4_p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on:         May 7, 2003, 15:25:19 ; Search time 92 seconds
                                        (without alignments)
                                        6505.818 Million cell updates/sec

Title:          US-09-965-830-1_COPY_6_3257
Perfect score:  6089
Sequence:       1 atgccggccatgcgggcct..........aagaaggcacaggggtctga 3252

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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
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Searched:       349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters:    698300

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 10%
                 Listing first 45 summaries

Command line parameters:
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Database : Published_Applications_AA:*
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(Summaries listing 1–45)

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 5    2461.5   40.4   1017   9   US-09-965-830-6         Sequence 6, Appli
 6    1901     31.2   1284   9   US-10-160-224-9         Sequence 9, Appli
 7    1901     31.2   1284  10   US-09-119-855-11        Sequence 11, Appl
 8    1835.5   30.1    542  10   US-09-119-855-5         Sequence 5, Appl
 9    1551     25.5   1159   9   US-10-000-151B-3        Sequence 3, Appli
10    1551     25.5   1159   9   US-10-193-692-5         Sequence 5, Appli
11    1551     25.5   1159   9   US-10-193-692-4         Sequence 4, Appli
12    1551     25.5   1159   9   US-09-735-995-2         Sequence 2, Appli
13    1551     25.5   1159  10   US-09-119-855-4         Sequence 4, Appli
14    1509.5   24.8   1159  10   US-09-119-855-10        Sequence 10, Appl
15    1487     24.4    994   9   US-10-192-440-8         Sequence 8, Appli
16    1486.5   24.4    290  10   US-09-119-855-8         Sequence 8, Appli
17    1475     24.2    958   9   US-10-188-308-24        Sequence 24, Appl
18    1432     23.5    960   9   US-10-188-308-21        Sequence 21, Appl
19    1405.5   23.1   1177   9   US-10-193-692-2         Sequence 2, Appl
20    1395.5   22.9   1186   9   US-10-192-440-10        Sequence 10, Appl
21    1378.5   22.6   1195   9   US-10-188-308-24        Sequence 24, Appl
22    1378     22.6    962   9   US-10-188-308-21        Sequence 21, Appl
23    1370.5   22.5    960   9   US-10-188-308-21        Sequence 21, Appl
24    1369     22.5    989   9   US-10-188-308-23        Sequence 23, Appl
25    1367.5   22.5    962   9   US-10-188-308-3         Sequence 3, Appli
26    1358.5   22.3    987   9   US-10-188-308-22        Sequence 22, Appl
27    1339.5   22.0    989   9   US-10-188-308-4         Sequence 4, Appli
28    1339.5   22.0    988   9   US-09-875-321-12        Sequence 12, Appl
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30    1332.5   21.9    988   9   US-09-875-321-5         Sequence 5, Appli
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34    536       8.8    521  10   US-10-188-308-22        Sequence 22, Appl
35    532       8.7    889   9   US-09-813-320-4         Sequence 4, Appli
36    531       8.7    875   9   US-10-067-457-1         Sequence 1, Appli
37    530       8.7    889   9   US-09-548-933-15        Sequence 15, Appl
38    513       8.4    863   9   US-09-548-933-2         Sequence 2, Appli
39    484       7.9    890   9   US-10-067-457-5         Sequence 5, Appli
40    484       7.9    890   9   US-10-158-684-4         Sequence 4, Appli
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42    475.5     7.8    774   9   US-10-158-684-10        Sequence 10, Appl
43    475.5     7.4    774   9   US-10-158-711-10        Sequence 10, Appl
44    449.5     7.4    749   9   US-09-548-933-1         Sequence 1, Appli
45    429.5     7.1    254  10   US-10-192-440-6         Sequence 6, Appl
      424.5     7.0    694   9   US-09-842-758-75        Sequence 75, Appl
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RESULT 1
US-09-965-830-2

; Sequence 2, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1083
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-965-830-2

Alignment Scores:
Pred. No.:
Score:                3.65e-275
Percent Similarity:   5704.00
Best Local Similarity: 100.00%
Query Match:          93.68%
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                              Matches:      1083
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SUMMARIES

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1	5704	93.7	1083	9		US-09-965-830-2	Sequence 2, Appli
2	5698	93.6	1083	9		US-10-160-224-1	Sequence 1, Appli
3	5659	92.9	1080	10		US-09-119-855-2	Sequence 2, Appli
4	5649.5	92.8	1082	9		US-10-121-746-20	Sequence 20, Appl

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Qy    41 ProValValTyrCysSerAspGlyPheCysAspSerLeuThrGlyPheSerArgAlaGluVal     60

Qy    61 MetGlnArgGlyLeuCysAlaCysSerProPheLeuTyrGlyProAspThrSerGluLeuArg     80

Qy    81 GlnGlnIleLeuArgLysAlaLeuLeuAspGluHisHisLysGluLeuIleLeuTyr         100

Qy   101 ArgLysSerGlyLeuProPheThrCysSerLeuLeuAspLeuProIleLeuLysGlnLys         120

Qy   121 GlyGluValAlaLeuAleuPheLeuValLeuSerHisLysAspPheIleSerGluThrArgLysAsnArgGly     140

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Qy   161 LysGlyGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisSerLeuHis     180

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Qy   201 AsnLeuProGlyIleTyrLysValAlaAlaIleArgSerProPheIleLeuLeuHisCys     220

Qy   221 GlyAlaLeuArgAlaThrArgAspGlyPheIleLeuLeuLeuAlaThrLeuTyrValAlaVal     240

Qy   241 ThrValProTyrSerValCysSerValSerThrAlaAlaArgGluProSerAlaAlaArgGlyPro     260

Qy   261 ProSerValCysSerAspLeuAlaValGluValLeuPheIleLeuGluLeuAspAsnPhe     280

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RESULT 2
US-10-160-224-1

; Sequence 1, Application US/10160224
; Publication No. US2003007731A1
; GENERAL INFORMATION:
;   APPLICANT: Jegla, Timothy J.
;   APPLICANT: Wickenden, Alan
;   APPLICANT: ICAgen, Incorporated
;   TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
;   FILE REFERENCE: 018512-0013200S
;   CURRENT APPLICATION NUMBER: US/10/160,224
;   CURRENT FILING DATE: 2002-05-28
;   PRIOR APPLICATION NUMBER: US/09/343,494
;   PRIOR FILING DATE: 1999-06-30
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 1
;   LENGTH: 1083
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human Elk (hElk; Eag (ether a go-go)-like K+ gene)
;   OTHER INFORMATION: potassium channel monomer protein
US-10-160-224-1

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-160-224-1 (1-1083)

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Score: 5698.00
Percent Similarity: 99.91%   Length: 1083
Best Local Similarity: 99.91%   Matches: 1082
Query Match: 93.58%   Conservative: 0
                                    Mismatches: 1
                                    Indels: 0
                                    Gaps: 0

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Db  161  LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
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Db  181  LeuGlnLysGlnProLysGlyLysHisLysGlnValPheGlyGluLysPro 200
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Qy  661  GGGGCACTGAGGAGCCACCTGGGATGGCCTTCATCCCTCGCCACACTCTAGCTGTGTC 720

Db  221  GlyAlaLeueuArgAlaThrTrpAspGlyPheIleLeuLeuLeuAlaThrLeuTyrValAlaVal 240
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Qy  721  ACTGTGCCCTACAGCGTGTGTGTGAGCACACGAGGACCCAGTGCCGCCCGGGCCCG 780

Db  241  ThrValProTyrTyrSerValCysValSerThrArgAlaArgGluProSerAlaAlaArgGlyPro 260
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Qy  781  CCCAGCGGTCTGTGACCTGGCCCGTGGAGGTGCCTTCTTCATCCCTTGTTGTGACTGT 840

Db  261  ProSerValCysAspLeuAlaValGluValLeuPheLeuLeuAspIleValLeuAsnPhe 280
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Qy  841  CGTACCACCATTCGTTCCTCAAGTCCGGGCCAGGTGGTGTTTGCCCCAAAGTCCATTT 900

Db  281  ArgThrThrPheValSerLeuLysSerGlyLnValValPheAlaProLysSerIleCysLeu 300
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Qy  901  CACTACGTCACCACTGGTTCCTGCTCAGTCATCGCAGCGCTGCCCCTTTGACCTGCTA 960

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Qy  961  CATGCCCTTCAAGGTCACGTAACGTGTACTTCGGGGGCCCATCGTCTGAAGAGCGTTG 1020

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Qy  1021 CGCCTGCTTGCCTGCCTTGCCTGCTCCGCGCGCTGGACCGGGTTACTCACAGCGCCGTGGTGCTG 1080

Db  341  ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
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Qy  1081 ACACTGCTCAATGGGCCGGTGTTCGCCCTGTCGCGTCTCGCGCACTGGCCTGCCCTGCT 1140

Db  361  ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
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Qy  1141 ATTTGGCCAGGGGAGATCGAGGACACGAATCCAGACGTGCCTGCCTGAGATTGGCTGGCTG 1200

Db  381  IleGlyGlnArgGluLeuGluSerGluSerGluLeuProGluLeuGlyTrpLeuGln 400
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Qy  1201 GAGCTGGCCCCGACTGGAGACTCCCTACTACTCGGTGGGCCCGAGGCCCAGCTGGAGG 1260

Db  401  GluLeuAlaArgAsgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
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Qy  1261 AACACTCCGGCCCGGACTGACAACTGCAGCAGCAGGCCAACGGGACGGGCTG 1320

Db  421  AsnSerSerGlyLnSerArgAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440
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Qy  1321 GAGCTGCTGGGCGGGCCCCGGCTGCCCAGCGCCGCCTACACATCCCTCTACTTCGCACTC 1380

Db  441  GluLeuLeuGlyLyProSerLeuArgSerAlaTyrIleThrThrSerLeuTyrPheAlaLeu 460
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Qy  1381 AGCAGGCCTCACCAGCGTGGGCCTTCGGCAAGCTGTCCGGCGCTACACAGCGACCAGAAGATC 1440

Db  461  SerSerLeuThrSerValGlyLyPheGlyAsnValSerAlaAsnThrAsgThrGlyLysIle 480
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Qy  1441 TTCTCCATCTGCACCATGCTCATCGGGCCCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1500

Db  481  PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500
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Qy  1501 ACGGCCCATCATCCAGTGCGATGTAGCGCCCGGCGTTTCTGTTACCACAGCGCAGCGAC 1560

Db  501  ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
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Qy  1561 CTGCGGCTGACTACATCCGCATCCCAAGCCCCTCAAGCAGGCCATGCTGGAG 1620
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Db  521  LeuArgAspTyrIleArgIleHisArgIleProLeuGlnArgMetLeuGlu 540
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Qy  1621 TACTTCCAGGCCACCTGGGCGTGGTGAACATGGATCGGATCGACACCACCGGAGCTGCAGAGC 1680

Db  541  TyrPheGlnAlaThrTrpAlaValAlaAsnAsnGlyIleAspThrThrGlyLeuLeuGlnSer 560
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Qy  1681 CTCCCTGACGAGCTGGCGCGGCAGACATCCCATGCCACCTGCCACAAAGGAGGTGCTCCAGCTG 1740

Db  561  LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
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Qy  1741 CCACTGTTTGAGGCCGGACCCAGCCGGCGCGGTCGCCTGGCCCACTGTCTCTGCGGCGCC 1800

Db  581  ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuLeuArgPro 600
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Qy  1801 TCCCTCCCACGCCGCGGGGGGAGTAACCTCATCCCACCAAAGGGCGATGCCCTGCAGGCCCTCTAC 1860

Db  601  AlaPheCysThrProGlyLeuTyrLeuIleHisGlnGlyLyAspAlaLeuGlnAlaLeuTyr 620
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Qy  1861 TTTGTTCTGTCTCTGGCTCCATGAGAGGGTGGCTTCCAGAGGTTGGGCAACGTGTCGCTCCCCATCCTAGG 1920

Db  621  PheValCysSerSerGlySerMetGluValValLeuLeuGlyGlyThrValLeuLeuAlaIleLeuLeuGly 640
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Qy  1921 AAGGGCGACCTGATCGGCTCGTGAGCGTGCCCGGCGGGCAGCAGGTGGTGAAAGGGCAATGCC 1980

Db  641  LysGlyAspLeuIleGlyCysGluGluLeuProArgArgGluGlnIleValValLysAlaLysAla 660
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Qy  1981 GACGTGAAAGGGGGCTGACGTACTACGCTGCGTCCTCGCCAGTGTCTCGCAGCTGCGCTGCGAC 2040

Db  661  AspValLysGlyLyLeuThrTyrCysValLeuGlnLeuGluGlyLyLeuHisAsp 680
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Qy  2041 AGCCCTTGCGCGTGTACCCCGACGTTTTGCCCGGCCCTTCAGTCGTGGCCTCCGAGGGGAGCTC 2100

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Qy  2101 AGCTACAAACCTGGGGTGTGGGGGAGGCGCTCTGCAGAGTGGGCACCAGCTCCCTGAGCGGC 2160

Db  701  SerTyrAsnLeuGlyValAlaGlyValGlyLyerAlaGluValAlaAspThrSerLeuSerGly 720
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Qy  2161 GACAATACCCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGGGAGGGCCACG 2220

Db  721  AspAsnThrLeuMetSerThrLeuGluLyGluThrAsgGlyGluGlnLnGlyProThr 740
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Qy  2221 GTCTCCCCAGCCCCCCAGCTTGATGAGCCCTCCAGCCCCCTGTCCTCCTGGCTCACCTCC 2280

Db  741  ValSerProAlaProGlyLeuLeuSerProSerLeuLeuLeuCysThrSer 760
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Qy  2281 TCATCCCTCAGCCTGCCAGCGTCTATCCCCACGTGTCGAACAGCACCCCGCCTCGTCTAGGT 2340

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Qy  2341 GGCAGAGGGAGGGCCAGGCAGGGGGCTTGAAGGCTGGAGGTCTGAGGGCCCCTGCTCCC 2400

Db  781  GlyArgGlyArgProGlyArgProGlyAlaGlyAlaAlaGlyValAlaGlyProSerAlaPro 800
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Qy  2401 CCACGGGCCCTAGAGGGCCTACGGCCTGCCCCAGCCATGGAAGAAGTGCCCCAGATCTG 2460

Db  801  ProArgGlyAlaLeuGluLeuGlyLeuArgLeuProProMetProTrpAsnValPro 820
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Qy  2461 AGCCCCAGGGTAGTAGAGTGCCATTGAAGACGACGCCCTCTGGCTCTCGGACGAGTTCT 2520

Db  821  SerProArgValValAspGlyIleGluGluAspGlyProLysPheSer 840
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Db  841  PheArgValGlyGlnSerGlyTyrGlyProSerSerSerProSerAspSerLyser 860
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Qy  2581 GGCCTGCCTCACTGTTCCCCATGGGCCCAGCCGACAAGGAGAACACAGAGCACACTGGACAAG 2640

Db  861  GlyLeuLeuThrValProHisGlyProSerGluAlaAlaArgAsnThrAspThrLeuAspLys 880
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Qy  2641 CTTCGGCAGGCGGGTGACAGAGCTGTCAGAGATGGGGGAGGACTGCAG 2700

Db  881  LeuArgGlnAlaAlaValThrGluLeuSerGluGlnValIleLeuGlnMetArgGluGluTyrLeuGln 900
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Qy  2641 CTGGCCGACTACATCCGCATCCCAAGCCCCTCAAGCAGGCCATGCTGGAG 2720
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Qy  2701  TCACTTCGCCAGGCCTGTGCCAAGCTTGTTCCTGGGGCCCCCAGGGGAGGAGGGTCCGGTGCCCTCGG  2760
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Db   901  SerIleuArgGlnAlaValGlnLeuValLeuAlaLeuAlaProHisArgGluGlyProCysProArg   920

Qy  2761  GCATCGGGAGAGGGGCCGTGCCCAGCCAGCACCTTCCGGGCTTCGTGCACGGCCGCTCTCCCGTGTG   2820
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Db   921  AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuValCysVal       940

Qy  2821  GACACTGGGGCATCCTCCTACTGCCTCGAGCCCCCAGCTGGCTCGTCGTGTTGAGGACT          2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   941  AspThrGlyAlaSerSerTyrCysLeuGluProProAlaGlySerValLeuSerGlyThr           960

Qy  2881  TGGCCCCACCCTCGTCCGGGGGCCTCTCCCCCTCCTGGGGGGTCCCCCA                      2940
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TrpProHisProAlaProGlyProProProLeuMetAlaProTrpTrpProGlyProPro           980

Qy  2941  GCGGTCTCAGAGCTCCCCTGGCCTCGACCCACAGCCTTTCTGGACCCCGCTCAGACTCA           3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981  AlaSerGlnSerSerProTrpProArgAlaThrAlaPheThrProHisSerThrSerAspSer       1000

Qy  3001  GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGACCCACCACCCTCCCCTCCTCCTCCT              3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1001  GluProProAlaSerGlyAspLeuCysSerAspProThrThrProLeuProSerProPro          1020

Qy  3061  TCTGAGGAAGGGGGCTAGGACTGGGGCCCCGCAGAGCCTGTGAGGCTGGCCTACCAGC             3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  SerGluGluGlyAlaArgThrGlyProProArgAlaGluProValSerGlnAlaGlyLeuThrSer    1040

Qy  3121  ACTGGAGAGAGCCCCCACCAGGGTTCAGGGGCCTGGCCTTGCCCTGGGACCCCCACAGCCTG         3180
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Db  1041  ThrGlyGluProProProGlySerGlyIleuLeuAlaLeuProLeuProAspProHisSerLeu      1060

Qy  3181  GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCCCCATCGTGGACCCAGGAAGAAGGC            3240
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Db  1061  GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGlyGly         1080

Qy  3241  ACAGGGGTC  3249
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Db  1081  ThrGlyVal  1083
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RESULT 3

US-09-119-855-2

; Sequence 2, Application US/09119855
; Patent NO. US200209197A1
; GENERAL INFORMATION:
;   APPLICANT: Curtis, Rory A.J.
;   TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;   FILE REFERENCE: mn1-055
;   CURRENT APPLICATION NUMBER: US/09/119,855
;   CURRENT FILING DATE: 1998-07-21
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 2
;   LENGTH: 1080
;   TYPE: PRT
;   ORGANISM: Monkey

US-09-119-855-2

US-09-965-830-1_copy_6_3257 (1-3252) x US-09-119-855-2 (1-1080)

Alignment Scores:
Pred. No.:   6.19e-273
Score: 5659.00
Percent Similarity: 99.63%   Length: 1080
Percent Identity: 99.54%   Matches: 1075
Best Local Similarity: 92.94%   Conservative: 1
Query Match: 10   Mismatches: 4
DB: 10   Indels: 0
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Qy    10  ATGCGGGGGCCCTCCTTGGCCGCCCTCAGAGAAACACCTTCCTGACACCATCGCTACGCCGTTCGAC   69
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Db     1  MetArgGlyLeuLeuLeuAlaProGluAsnThrPheLeuAspThrIleAlaThrArgPheAsp       20

Qy    70  GGCACGGCACAGTAAACTTCGGTGCTCAGGTGCTGGGGCAAGCGCCCCAGGTGGGGGGCTCTTTCCCGGTGTC  129
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21  GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPheProValVal            40

Qy   130  TACTGCTCTCTGATGGCTTCTGTGGACCCTCACGGCGCTTCTCCCCGGGCGAGGTCANTGCAGCGG       189
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  TyrCysSerLeuMetAlaSerValAspProHisGlyAlaSerProArgAlaGluValMetGlnArg      60

Qy   190  GGCTGTGCCCTGCTCCTTTTTCTTTATGGGCCAGACACCAGTGAGGTCGCCGCCAACAGATC         249
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GlyCysAlaCysSerProPheLeuPheLeuTyrGlyProAspThrSerGluValAlaAlaAsn        80

Qy   250  CGCAAGGCCCCTGGACGAGCACAAGAGAGTTCAAGGCGTGATCCTGTACCGGGAGAGC             309
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  ArgLysAlaProGlyArgAlaGlnGluSerSerArgArgAspProValTyrArgGluSer          100

Qy   310  GGGCTCCCGGTTCTGGTGTCTCCTGGATGTGATATACCGGATAAAGAAATGAGAAAGGGGAGGTG      369
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Db   101  GlyLeuProPheLeuValSerProGlyCysAspIleProAspLysGluMetArgLysGlyArgVal     120

Qy   370  GCTCTCTTCCCTAGTCTCTCACAAAGGACATCAGCGAAACAACCAAGAAAACCGAGGGGCCCGAC      429
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AlaLeuPheLeuValLeuSerHisLysAspIleSerGluThrThrLysLysThrGluGlyProAsp     140

Qy   430  AGATCGGAAGGAGACAAGTGTGGCCGCGGCGGCGACGATCATGGGCGGGCGACGATCCAAAGGCTTC    489
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Db   141  ArgSerGluGlyAspLysCysGlyArgGlyGlyAspAspHisGlyArgAlaThrIleGlnArgLeu     160

Qy   490  AATGCCAACCGGGCGGAGCCCAGTGCGCCGGCCGTGCTCAAGCTGTCCAGGCACCTGTCCGAGAAG    549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161  AsnAlaAsnArgAlaGluProSerAlaProAlaValLeuLysLeuSerArgHisLeuSerGluLys     180

Qy   550  CAGCCCAGGGCAAGCACAAGCTCAATAAGGGGTGTGTTTGGGGAGAAAACCAAACTTGCCT         609
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Db   181  GlnProArgGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysThrLysLeuAlaLeu        200

Qy   610  GAGTACAAAGTAGCCGCCATCCGGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGGCACTG         669
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Db   201  GluTyrLysValAlaAlaIleArgGluValAlaLeuHisProValAla                      220

Qy   670  AGAGCCACCTGGGAGTGGGCTTCAtCCTGGTCGCGCACACTCTATGTGCCGTCCACTGTGCC         729
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Db   221  ArgAlaThrTrpGluTrpAlaPheLeuLeuValAlaHisThrLeuTyrValAlaValThrValPro    240

Qy   730  TACAGCCGTGTGTGTGAGCACAGCAGCGAGCCCAGTGCGCCGGCCGTGCTCCAGCGGTC            789
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Db   241  TyrSerValCysValSerThrAlaAlaGluProSerAlaProAlaValLeuGlnProSerVal        260

Qy   790  TGTGACCTGGCCCGTGGAGGTCCTCCTTCAtCCTTGACATTGTGCTGAATTTCCGTACCACCA       849
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Db   261  CysAspLeuAlaArgGlyGlyProValProLeuPheIleLeuAspIleValLeuAsnPheArgThr    280

Qy   850  TTCGTGTCCCAACTCGGGCCCAGTGTTGTTGCCCAAAAGTCAtTTGCCTCGTACGTC             909
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Db   281  PheValSerLysSerGlyValGlnValValAlaGlnLysSerLeuAlaSerTyrVal             300

Qy   910  ACCACCTGGGTTCCTGCTGGAtTTCAtCGGCTACAtTGCCC                              969
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Qy   970  AAGGTCAACGTGTACTTCGGGGCGGCCCCAAtCTGCTGAAGACGGTCGCGCGCCTGCCGCTG         1029
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Db   321  LysValAsnValTyrPheGlyAlaAlaHisIleLeuLysThrValAlaArgLeuLeuLeu           340

Qy  1030  CGCCTGCTTCCGCGGCCGTGACCGGTACTCGAGTACAGCCGTGGTGGTGCTGACTCCTC           1089
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Db   341  ArgLeuLeuProArgProValThrGlyTyrSerArgAlaValValLeuThrLeuLeu              360

Qy  1090  ATGGCCGTGTTCGCCCTGCTCGGCGCACTGGGTCCGTCGGTTTTAAttGGCCAG                1149
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Db   361  MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyTyrGln       380

Qy  1150  CGGGAGATCGAGAGCACGGAATCCGAGCTGCCCTGAGAtTGGCTGCTGCAGGAGGTGGCC          1209
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Qy    381 ArgGlnIleGluSerGluSerGluProLeuThrLeuAla 400
          ||||||||||||||||||||||||||||||||||||||||
Db   1210 CGCGGACTGGAGAGCCCTACTACCTGGTGTGGGCCGGAGGGAACAGTCC 1269

Qy    401 ArgArgLeuGlyThrProTyrTyrLeuValGlyArgArgProLeuGlyGlyAsnSerSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 GGCCAGAGTGACAACTGCAGCGACAGCAGCAGGGCCAACGGGCTGGGAGCTGCTG 1329

Qy    421 GlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyLeuGlyLeuLeu 440
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Db   1330 GGCCCCAGGTTCGGTCCGCCCTACACCATGCCCGGAGAAGATCTTCTCCATC 1389

Qy    441 GlyGlyProSerAlaTyrIleThrSerLeuThrTyrPheAlaLeuSerSerLeu 460
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Db   1390 ACCAGCGTGGGCTTCGGCAAGTGTCCGGCCAACACCGAGAAGATCTTCTCCATC 1449

Qy    461 ThrSerValGlyPheGlyLysCysProAlaAsnThrAspThrGluIlePheSerIle 480
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Db   1450 TGCACCAGCGTCATCGGCCCTGATCGCACCCGGTGGTGTTTGGGACGTGACGGCCATC 1509

Qy    481 CysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIle 500
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Db   1510 ATCCAGGCCATGATACGCCCCGGCCTTTCTGTACCACAGCCCGCCACCTGCCCGAC 1569

Qy    501 IleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAspLeuArgAsp 520
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Db   1570 TACATCCGCTATCCCAAGCCCCCTTCAAGCTCGAGTACTTCAG 1629

Qy    521 TyrIleArgIleHisArgIleProLysProLeuGlyArgMetLeuGlyTyrPheGln 540
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Db   1630 GCCACCTGGCGGGTGAACAATGGCATCGACACCCCAGGCTCAGAGCCTTCTGAC 1689

Qy    541 AlaThrThrArgAlaValAlaAsnAsnGlyIleAspThrThrGlnLeuLeuGlnSerLeuProAsp 560
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Qy   1690 GlyLeuLysTyrLeuIleHisGlnGlyAspAlaLeuLeuTyrPheValCys 620
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Db    561 GluLeuArgValAlaAspIleAlaMetHisLeuHisLysGluValLeuProLeuPhe 580

Qy   1870 SerGlySerMetGluValLeuLeuLysGlyLyThrValLeuAlaIleLeuLeuGlyLysGlyAsp 640
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Qy   1810 AccGCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCTGTACTTTGTCTGT 1869
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; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030035648Ale1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR APPLICATION FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1082
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-20

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Score:                  5649.50
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Best Local Similarity:  99.35%
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                        Mismatches:     6
                        Indels:         1
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US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-121-746-20 (1-1082)

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Db      1 MetProAlaMetArgGlyLeuLeuArgProGlnAsnThrPheLeuAspHisArgTyrAlaThr 20

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCGTTGCTGGGCAACGCCCAGGTGGCGGGGGCTCTTC 120
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Db     21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaSer---GlyGlyAlaLeu 39

Qy    121 CCCGTGGTCTCTACTGCGCTCTGAGGGCTTCTGTGACCTCACGGGGCGTTCTCCCGGGCTGT 180
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Qy    181 ATGCACGGGGGCCTGTGCCCTCGCTGCCTTCCTTTATGGGGCCAGACACCACTGAGTCTCCGC 240
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Qy    301 CGGAAGAGCGGGGCCTCCCGGTTCTGGTGTCTCGGATGGTGATACCCATAAAGAATGAGAAA 360
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Qy    361 GGGGAGGTGGCCTCTCTCTTCTCAGTCTCTCACAAGGACATCAGCGGAACCAAGAACCGAGGG 420
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Qy    421 GGCCCCGACGACATGGAAGGACAGGTGGTGCGGCCGCGATAGGGCGCACGAATCC 480
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Qy    481 AAAGGCTTCAATGCCAACCGACGGCGGGAGCCGGCGCCCGTGCTCTACCACTGTCCGGGCAC 540
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Db    160 LysGlyPheAsnAlaAsnArgArgArgGluProAlaAlaValLeuTyrHisLeuSerGlyHis 179

Qy    541 CTGCAGAGAGCAGCCCAAGCACACAATATAAGGGGTGGTGTTTGGGGAGAAAACCA 600
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Qy    601 AACTTGCCTGAGTACAAAGTAGCCCCCATCCGGAAGTCCCCTTCATCGCTGTGT 660
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Qy    661 GGGGGCGACTGAGAGCCACACCTGGGAATGGCTTCATCCTGCTGCTGCACACTCTATGTGCCGTC 720
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Qy    721 ACTGTGCCCTACACGCTGTGTGTCGAGCACAGCACAGGGAGCCCGCGGCCCCG 780
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Qy    781 CCCAGGCTGTCTGACCTGGCCGTGGGCGGAGGTCCCCTTCATCCTTGACATTGTGCTGAATTTC 840
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Db    260 ProSerValCysAspLeuAlaValGluValLeuProPheIleLeuAspIleValLeuAsnPhe 279

Qy    841 CGTACCCACATTCGTTCGTAGCCAAAGTCGGGCCCAGGTGGTGTTGGCCCAAAGTCCAATTGCCTC 900
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Qy   1021 CGCCTGCTTGCGCCTTGCTTCTCCCGCGGCTTGGGACCGGTTACTCAGTACTACAGCGCTGTGCTG 1080
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Qy   1081 ACAACTGCTTCAAGGGCCCTGTGTTCGCCCTGCTTCGGCCACTGGGTCGCCGTCGCTGCTGGTTTTAC 1140
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Db    360 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaLaHisTrpValAlaCysValTrpPheTyr 379

Qy   1141 ATTGGGCAGCGCGGGAGATCGAGACAGCACGGAATCCGAGACTGCTGAAGAAAATTGGCTGGCTGGAG 1200
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Db    380 IleGlyGlnArgGluIleGluSerGluSerGluLeuProGlyIleLeuGlyTrpLeuGln 399

Qy   1201 GAGCTGCTGGGCGCCGCGTCGCGCTGGGAGACTCCCTACTTACCTGGTCGGGCCGGAGGG 1260
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Db    400 GluLeuGlyArgArgLeuGluThrProTyrLeuProValValGlyArgArgProAlaGlyGly 419

Qy   1261 AACAGCTCCGGCACAGAGTGACAACTGCAGCAGCACGAGGGCCAACGGAGCCCTG 1320
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Db    420 AsnSerSerGlyGlnSerAsnCysSerSerGluAlaAsnGlyThrGlyGly 439

Qy   1321 GAGCTGCTGGGCGCCGCGTCGCGCTGGGAGCCCTACACATCACCTCCCTCTACTTCGCACTC 1380
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Qy   1381 AGCAGCCTCACCAGCGTGGGGCTTCGGCCAACGTGTCCGCCAACAGGGACACCGAGAAGATC 1440
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Qy   1441 TCTCCACATCTGCACCATTCTCATCGCGCCCTGATCGCAGTGCACGCGGGTTGGTGTTTGGGAACGTG 1500
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Qy   1501 ACGGCCATCATCCAGGCCAGTAGTACGCCCCGCGCTTTCTGTACCACAGCGCCACGGCGCAC 1560
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Qy   1561 CTGCGCGACTACATCCGCTGTATCTCCCAAGCCCTCAGCAGCAGCGCATGGGAG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1861 TTTGTTCTGCTCTTCGGCCATCAAGGAGTGTCAAGGGTCGTTCCACATCCTAGG  1920
Db  620  PheValCysSerGlySerMetGluValLeuLysLysGlyGlyThrValLeuLeuLleLeuGly  639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 AAGGGCGACCTGATCGGCGTCGTGCCTGAGCGTCCCCGGGGCGGCAGGTGGCCAATGCC  1980
Db  640  LysGlyAspLeuIleGlyCysGluLeuProArgProArgGlyGlnValValLysAlaAsnAla  659
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 GACGTGAAGGGGCTGACGTACTGCGTTCCTCGCAGTGTCTCCAGTGGCCTGCCCTCGACGAC  2040
Db  660  AspValLysGlyLeuThrTyrCysValLeuGlnCysSerGluGlnIleAlaGlyLeuHisAsp  679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041 AGCCTTGGCCGTGTTACCCCGAGTTTCGCCGCGCCGCTTCAGTTGGCTGGCCTTCCAGGGGAGTC  2100
Db  680  SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu  699
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101 AGCTACAAACCTGGGGTGCTGGGGAGGTGGACACCAGCTCCTGACGGC  2160
Db  700  SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly  719
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 GACAATACCCTTATGTCCACCCTGGAGGAGAAGAGACAGATGGGGAGACAGGGCCCCACG  2220
Db  720  AspAsnThrLeuMetSerThrLeuGluGluLysArgGlnMetGlyGlyGlnGlyProThr  739
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 GTCTCCCCAGCCCAGCTGATGAGCGCCTTCAGGCCCTCAGGCCCCTGCTGCTGCCCTCC  2280
Db  740  ValSerProLeuAlaProLeuAlaSpGluProSerLeuLeuSerProGlyCysThrSer  759
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 TCATCCTCAGCTGCTATCCCCACGTCGAACAGACACCCGGACCTGCTCTAGGT  2340
Db  760  SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProLeuGly  779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 GGCAGAGGGAGGGCCAGGCGAGGGCTTTGAAGGCTGAGGCTGGCCCCCTGTGCTCCC  2400
Db  780  GlyArgGlyArgProGlyArgAlaGlyValAlaGlyLeuAlaGlyProSerAlaPro  799
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 CCACGGCGCCCTAGAGGGGCTACGGCTGCCCCCATGCCAATGTGCCCCCAGATCTG  2460
Db  800  ProArgAlaLeuGluGlyLeuArgLeuProMetProTrpAsnValProProAspLeu  819
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 AGCCCCAGGGTAGTAGAGATTGAGACACGGCTGTGGCTGCCTCGACCAAGTTTCTCT  2520
Db  820  SerProArgValValAspGlyIleGluIleAspPheGlyCysGlySerAspSerGlnProLysPheSer  839
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 TTCCGCGTGGGGCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCCCTGACAGAGC  2580
Db  840  PheArgValGlyGlnSerGlyProGluCysSerSerSerProGluGlnGluGlu  859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 GGCCTGCTCCACTGTTCCCCACGGCAAGAGAACACAGACACACTGACAAG  2640
Db  860  GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys  879
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 CTTCCGGCAGCGCGGTGACAGAGCTGTCGAGATGCGGGGAAGGGAGGAGACTGCAG  2700
Db  880  LeuArgGlnAlaValThrThrGluLeuGlnValLeuGlnMetArgGlyLeuGln  899
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 TCACTGCTTCGCCACTGTTCTCCTGGCGCCCACAGGGAGGGTTCGGTGCCCTCGG  2760
Db  900  SerLeuLeuArgHisValLeuAlaProHisSerArgGluGlyLeuProCysProArg  919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761 GCATCGGGAGAGGGGCCGTGCCCAGCCAACCTTCCGGCTTCTGCAGCCCTGTCTGTG  2820
         ||||||||||
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Db  920  AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal  939
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 GACACTGGGGGCAATCCTCCTTCCTACTGTGCCTGCCAGCCCCCAGCCTGCCTCTGTGCTGGGGACT  2880
Db  940  AspThrGlyAlaSerSerTyrCysGluGlnLeuProProAlaGlySerValLeuSerGlyThr  959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881 TGGGCCCACCCTCGTCCTGGGGGCGGCCTCCTCCCATGGGCACCCTCGGGGTCCCCA  2940
Db  960  TrpProHisProArgProGlyProProLeuMetAlaProArgProTrpGlyProPro  979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941 GCGTCTCAGAGCCTCCCCCCTGCCCTCGAGCCACAGTCTTCTGGACCTCCACCTTCAGACTCA  3000
Db  980  AlaSerGlnSerSerProThrProArgAlaThrAlaPheThrProThrSerAspSer  999
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 GAGCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTGCCTCCCCCTCCT  3060
Db  1000 GluProProAlaSerGlyAlaAspLeuCysSerGluProSerGlnThrProAlaSerProPro  1019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 TCTGAGCAGAAGGGGCCTAGGACTGGGGCCCGCAGAGGCGGTGCTGAGGCTACCAGC  3120
Db  1020 SerGluGlyLyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer  1039
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 ACTGGAGAGCCCCCACCAGAGGTCAGGGGGACGGGGGGGCGGGGGGGGAGCCTG  3180
Db  1040 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuGluLeuProThrAlaProSerLeu  1059
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181 GAGAATGGTTGCCTTAATTGGGCTGGCCATGGCCGTCTGGCACGGTCCAGTGGACCCAGGAGAAGC  3240
Db  1060 GluMetValLeuIleGlyCysHisSerGlySerGlyThrValGlnTrpThrGlnGluGly  1079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 ACAGGGGTC  3249
Db  1080 ThrGlyVal  1082
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RESULT 5
US-09-965-830-6
; Sequence 6, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
;   APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;   TITLE OF INVENTION: A novel potassium channel protein
;   FILE REFERENCE: Y9903-PCT
;   CURRENT APPLICATION NUMBER: US/09/965,830
;   CURRENT FILING DATE: 2001-10-01
;   PRIOR APPLICATION NUMBER: 09/600,776
;   PRIOR FILING DATE: 2001-07-21
;   PRIOR APPLICATION NUMBER: JP P1998-346198
;   PRIOR FILING DATE: 1998-12-04
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 6
;   TYPE: PRT
;   LENGTH: 1017
;   ORGANISM: Homo sapiens
US-09-965-830-6
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Alignment Scores:
Pred. No.:                         1
Score:                       2461.50
Percent Similarity:           59.19%
Best Local Similarity:        48.47%
Query Match:                  40.43%
DB:

Length:     1017            1.45e-114
Matches:     538
Conservative: 119
Mismatches:  245
Indels:      208
Gaps:         23            9
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US-09-965-830-1_Copy_6_3257 (1-3252) x US-09-965-830-6 (1-1017)

Qy    1  ATGCCGGCCATGCGGGGGCCTCGGCCGCCTCAGACAACACTTCCTGGACACAATCGCCTACG  60
         ||| || ||           ||:::||| |||  ||| | |  | |||||| || ||| || |
Db    1  MetProValMetGlyLeuLeuAlaProGlnAsnThrPheLeuAsnAspThrIleAlaThr  20

Qy   61  CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGGGCTCTTC  120
         ||||||||||||||||||||:::|||||||||||||||::||||||||||||||| |||
Db   21  ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnInGlyThrArgGlyPhe  40
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Qy    121 CCCGTTGGTTCTACTGCTTCTTGTGACTCGATGGGGCTTCTCCCGGGGCTGAGGTC 180
          ||||:::|||||           |||||       |||||         |||||
Db     41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrArgIleTyrGlyArgThrGluVal 60

Qy    181 ATGCAGCGGCGCTGTCCTGCTTCCTTTATTGGGCAGCCAGTGACCTCGTCCGC 240
          ||||| ||||:::|||       |||||||||||        ::|||
Db     61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyArgGlyProAlaLeu 80

Qy    241 CAACAGATTCCGACAAGGCCCTTGGACAGCACAAGAGAGTTCAAGGCTGAGCTGAGCTCTGTAC 300
          |||||            |||||           ||||||         |||||
Db     81 GlnArgIleHisLysAlaLeuGluGlyLysHisGlnGluHisArgAlaGlnIleIleCysPheTyr 100

Qy    301 CGGAGAGGTGGCTCCCGTTCTGGGTGATACCCATAAAGAATGAGAAA 360
          |||||        |||||       ||||| |||||          |||||
Db    101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetProIleLysAsnGluMet 120

Qy    361 GGGGAGGGTGGCTCTCCTTCCTTAGTCTCACAAGGACATCAGCGAAACCAAGAACCGAGG 420
          |||||   |||||        ||||||     ::::|||
Db    121 GlyGluValValLeuPheLeuPheSerHisGlyArgGlnGlnSerGlySerProGly 140

Qy    421 --GGCCCGACAGAATGGGAGGAGGACAGGTGGTGGCCGGCGCCGATATGGCCGGGCACGA 477
                     ||||||          |||||
Db    141 --GlyGlyGlyGGTGTTTCGGGAGGAAACCAAACTTGCCCTGAGTACACCAGGCCCATCCGGAAG 194

Qy    478 TCCAAAGGC----------TTCAATGCCAACCACGGCCTCTCCCGGAGCCGGGCC 516
          |||::|||          |||||
Db    195 AsnAsnValPheGluProLysProSerValProGluTyrLysLysValAlaLeuValGlyGly 214

Qy    517 GTGGTCTACCACCTGTTCCCGGCACCTGAGCACCTGAGGCACCACAAGCTCAAT 576
          |||||         |||||      :::|||
Db    215 SerArgCysLeuLeuLeuHisLeuHisSerTyrSerValSerLeuSerLysAlaIleTrpAspProGlyTyrLeuLeu 234

Qy    577 AAGGGGGTGTTTCGGGAGGAAACCAAACTTGCCCTGAGTACACCAGGCCCATCCGGAAG 636
          |||||||        ||||||      |||||
Db    235 LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerSerGlyAspAsp 254

Qy    637 TCGCCCTTCATCCTGTTGACCTGTGGGGATGGCTTCATCCTG 696
          |||||           |||||        |||||
Db    255 AspThrProIleLeuThrSerArgHisThrLeuValSerArgAspIleAlaValGlyMetLeuPhe 274

Qy    697 CTCGCCACACTCTATGTGGGGCGTGTCACTGTGCCACGCACACACACG 756
          |||||            ||||||          |||||
Db    275 IleLeuLeuAspIleLeuIleLeuLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValIle 294

Qy    757 GAGCCCAGTGCGCCCCGCCCGCCTGTCGACCTGGGAGGTCCTCTTC 816
          |||||        |||||       |||||
Db    295 GluProSerAlaProArgProProValAspLeuGlyGlyProProPhe 314

Qy    817 ATCCTTGACATTGTGCTGAATTCCGTACCACATTGGCTGCTACCAGGTGTTCC 876
          |||||         |||||        |||||
Db    315 AlaAlaLeuProPheAsnSerValThrHisTrpLeuLeuProGlyValSer 334

Qy    877 TTTGCCCCAAAGTCATTGCCCTACTAGCTCAGGTTCCTGCTGGATGTCATC 936
          |||||         |||||          |||||
Db    335 LeuLeuLysThrValAlaLeuLeuAlaGlnValProAlaGlyCysHis 354

Qy    937 GCAGGGCCTGCCCTTGAACTGCTACAATGGCTCAACGTGACTACTTCGGGCCCAT 996
          |||||         |||||        |||||
Db    355 SerGlnCysSerAlaValValLeuThrLeuGlnMetSerValPheAlaAlaLeuLeuAlaHis 374

Qy    997 CTGCTGAAGCACGGTGTCGCGCCTGCCTGCCTTGTTTCCGGACCGGTAC 1056
          |||||         |||||        |||||
Db    335 AlaAlaAlaLeuProPheAsnSerIleThrValThrSerLeuValHis 334

Qy   1057 TCCGAGTACGACAGGCGGCCGTGCTGACACTGTTCGGCGTCGCCGCAC 1116
          |||||         :::|||        |||||
Db    355 LeuLeuLysThrValAlaArgLeuLeuAlaArgLeuLeuGlnLeuSerLeuGluArgThrTyr 354

Qy   1117 TGGGTCGCGTCGCCGCTGCTGTTTTTACATTGGCCACGGGGGATCGGAGACGAATCCCGAG 1176
          |||:::||:||||||    ||||| |||||
Db    375 TrpMetAlaCysIleLeuThrTyrValIleLeuGlyTyrArgArgGluMetGluAlaAsnAspProLeu 394
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Qy   1177 CTGCCTGAGATTGGCTCGTGGGCTGTGCCAGGAGTCTGGCCGCCGACTGGAGACTCCTACTG 1236
          ||||            :::||||||           ||||:::|||||
Db    395 LeuTrpProAspProIleGlyLeuTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr------ 412

Qy   1237 GTGGGCCGGAGGCCAGCTGGAGGGAACAGCTGCGCGGCCCAGAGTGACACGTGACAACTGCAGAGCAGC 1296
          ||||||
Db    412 ------------------------------------------------------------------- 412

Qy   1297 ACGGAGGGCCAACGGCGACGGGCCTTGGAGCTGCTGGGCCCCGTCGCTGCCCGCACGGGCCTAC 1356
          |||||           |||||        :::|||
Db    413 -----------------ValAsnGlySer----------ValGlyGlyProSerArgArgSerAlaTyr 426

Qy   1357 ATCACCTCCCTCTTACTTCGCCACTCAGCACGCCTCACCACCGCGTGGGGCTGGGCTTCGGGGAAG 1416
          |||||||       :::|||          |||||
Db    427 IleAlaLeuAlaLeuGluTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys 446

Qy   1417 GCCAACACGGACACCGAGAAGATCTCCACTGCCATCCACATCTCATCGGGGCCTGATG 1476
          |||||          |||||        |||||
Db    447 AlaAsnThrAspThrGluLysIlePheSerSerIleCysThrAlaIleHisSerGlyIle 466

Qy   1477 CACGCGGTGGTGTTTGGGAACGGTGACGGCCCATCAGCGACATGTACGCCCCGCGCTTT 1536
          |||||         |||||         :::|||
Db    467 HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer 486

Qy   1537 CTGTACCACAGCGCGCACGCGCCGGCGACCTGCCGCGACTACATCCGCATCCCAAAG 1596
          |||||          |||||
Db    487 LeuTyrHisSerArgMetLysAspLeuProLeuLeuArgAspPheLeuArgIleProArg 506

Qy   1597 CCCCTCAAGCAGGCGCAGCTGGAGTACTTCAGGACAGGCTGGAAATGGCATC 1656
          |||||         |||||
Db    507 ProLeuLysGlnAlaGlnLeuGluTyrPheArgThrGlyTrpLysTrpProAlaValAsnSerGlyIle 526

Qy   1657 GACACCAACCGAGCTGCTGCAGAGCTCCCTCGCACGACGTAGCCTTCCTACCTCATCCACCAA 1716
          |||||       ||||| |||||
Db    527 AspProAlaAsnGluHisIleIleLeuTyrSerPheCysArgAlaProGlyLeuTyrLeuLeuArgArgAsp 546

Qy   1717 CTGCACAAGGAGGTCCTGACCACTGCCAGCTGGCCGTTGAGGCGGCCAGCCGGCTGCCGTGCG 1776
          |||||        |||||
Db    547 LeuLeuAsnArgGluIleLeuLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArg 566

Qy   1777 GCACTGTCTCTGCCCTCGGGCCCTGCGGGCCCCCCCTCTTGCACGGCGGAGTACCTCATCCACCAA 1836
          |||||       :::|||      :::|||
Db    567 AlaLeuSerLeuHisIleIleLeuTyrSerPheCysArgAlaProGlyLeuTyrLeuLeuArgArg 586

Qy   1837 GGCGATGCCCTGCCAGGCCCATCCTACTTTGTCTGCTGGGCCTCCAGGGT 1896
          |||||       :::|||
Db    587 GlyAspAlaLeuGlnAlaHisIleTyrPheValCysSerGlyLeuValLeuLeuArgAsp 606

Qy   1897 GGCACCGTGCTCGCCCATCCTAGGGAAGGCGACACTGTGCCCCGGCGG 1956
          |||||       :::|||
Db    607 AsnMetValLeuLeuAlaIleLeuGluGlyLysGlyAlaAspIleProGluPro 626

Qy   1957 GAGCAG------------GTGGTAAAGGGCCAATGCGACGTG 1986
          |||
Db    627 GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLeuGlyThrSerAlaAspVal 646

Qy   1987 AAGGGGCTGACGTACTGCGGTGCTGGTCTCGCAGTCGACACAGCCCTT 2046
          |||||||         |||||
Db    647 LysGlyAlaLeuThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuValLeuAlaGluValLeu 666

Qy   2047 GCGCTGTACCCCGAGTTTGCCCCGCGTCGCGTGGCCTTCAGTGGTCGCCAGGTAC 2106
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Db    667 ArgGlyLeuTyrProGluTyrGlyValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686

Qy   2107 AACCTGGGGTGCTGGGGAGGCTCTGCAGAGGTGACACCAGTCCCTG----- 2154
          |||||:::|||
Db    687 AsnLeuArgGlnGlySer---------AspThrSerGlyLeuSerArgPheSer 701

Qy   2155 ------------------AGGGGGACAAATACC 2169
                           |||
Db    702 ArgSerProArgLeuSerGlnProArgGluSerLeuGluGlySerLeuGluGlySerSerSerAspLysThr 721

Qy   2170 CTTATGTCCACGCTGGAGGACGAAGGAGACAGGCGCCCACGGTCTCCCCA 2229
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RESULT 6
US-10-160-224-9

; Sequence 9, Application US/10160224
; Publication No. US20030077731A1
; GENERAL INFORMATION:
;    APPLICANT: Jegla, Timothy J.
;    APPLICANT: Wickenden, Alan
;    APPLICANT: ICAgen, Incorporated
;    TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
;    FILE REFERENCE: 018512-0013200US
;    CURRENT APPLICATION NUMBER: US/10/160,224
;    CURRENT FILING DATE: 2002-05-28
;    PRIOR APPLICATION NUMBER: US/09/343,494
;    PRIOR FILING DATE: 1999-06-30
;    NUMBER OF SEQ ID NOS: 9
;    SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;    LENGTH: 1284
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
;    FEATURE:
;    OTHER INFORMATION: Drosophila Elk (dElk; Eag (ether a go-go)-like K+
;    OTHER INFORMATION: gene) protein
US-10-160-224-9

US-09-965-830-1_copy_6_3257 (1-3252) x US-10-160-224-9 (1-1284)

Alignment Scores:
Pred. No. :
Score:                     8.52e-87
                           1901.00
Percent Similarity:        53.85%           Length:          1284
Best Local Similarity:     40.77%           Matches:          455
Query Match:               31.22%           Conservative:     146
DB::                       9                Mismatches:       273
                                            Indels:           242
                                            Gaps:              31

Qy     1 ATGCCAGCGGGGCCATGCGGGGGCGCCTCCTGGCCGCTCAGAGAACACCTTCCTGGACACCATCGGCTACG 70
         |||||||||   ||::||||||||||||::|:|||||       |||     |||||::|||::||||||||
Db     1 MetProAlaArgLysGlyLeuLeuLeuAlaAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy    61 CGGCTTCGACGGCAGGCACGCACAGTAACTTCGTGGCCAAGCCCAGGTGGCGGGGGGTCTTC 120
         |||||||||||:||||||||||||||::::::||||||||||||||||||||||||||||||
Db    21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAlaAlaGlnAlaSerGly---Asn 39

Qy   121 CCCGTGGTCTACTGCCTCTGATGGGTTCTGTGACCTCACGGGCTTCTCCGGGGCTGAGGTC 180
         ||::||||||||||||||::||||:||||||||||||||:|||||||:|||:||||:::::
Db    40 ProIleValTyrCysSerAspGlyPheValAspSerLeuThrGlyTyrSerArgAlaGlnIle 59

Qy   181 ATGCACGGGGGCTGTGCCCTGCCTGCTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC 240
         |||:|||||||:||::||||||:|||||||||||||||||||||||||:||||||:||:||
Db    60 MetHisGlyGlyCysAlaLeuProAlaProLeuTrpAlaArgHisGlnEnd 79

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         |||:|||||||:|:|||||||||||||||||||:|||||||||||||||||::|||||||||||
Db    80 GlnGlnIleGlyGluGlyProTrpThrThrHisThrArgSerSerArgLeuSerGluValIlePheTyr 99

Qy   301 CGGAGAAGCGGGGGCGCTTCCCGTTCGTGGGTGTCCTCGGGATGTGTAATGCGTCCCCCAGTAAGAATGAGAAA 360
         |||||||||||||||:|||||||||||||||||||:|||||||:||||||||::||||::|||||||||||
Db   120 ArgArgAspAspValValLeuProPheGlyValGluProHisHisLysMetLeuGlu 139

Qy   361 GGGGAGGTGGGCTCTCTTCCTAGTCTCTCCACAAGGACATCACGGAAACCAAG 411
         |||||||||||:||||||||||||||||:|||||||||||||||:::||||
Db   140 MetAsnValAsnGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyLeuAla 159

Qy   412 ----ArgPheArgAlaGlySerIleLeuProTyrTyrSerGluPr 471
            |||:|||||||||||||||||||||||||||||||:|||
Db   160 ------GACAGATGGAAGGAGGAGGACGAAGGTGGTGGCGGCGGGCGGCGGGATATGGCCGG 179

Qy   946 oCysProGln----LeuArg----ProProCysLeuSerProCysAlaSerArgProPr 995
                |||::|||:||:||::|||:|||||:|||:||
Db   180 GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro 199

Qy  2290 GCTGCCAAGCTG 2301
          |||
Db   722 LeuProSerIle--------ThrGluAlaGluSerGly------AlaGluPro 734

Qy  2230 GCCCCAGCTGATGAGCCTTCCAGCCCCTGCGTTCCCCTGGCTGCACCTTCTCATCCTCA 2289
          |||:||       |||||||||       |||||||||||||
Db   735 GlyGlyGlyProArgProArgArgProLeuLeuAsnLeuSerProAlaArgPro 754

Qy  2302 ----CTATCCCACGTCGAACAGACAACCCCTTCGTTCCTGGCAGGAGAGGAGG 2352
              |||||||:||||:||||||||:||::|||
Db   755 ArgGlySerLeuValSerLeuLeuGlyGluGluLeuProProPheSerAlaLeuValSer 774

Qy  2413 GAGGGG------------- 2412
          ||:::|
Db   792 gGluLeuArgHisIleMetGlyLeuLeu 802

Qy  2353 CCAGGCAGGGGCAGGGGCTTTGAAGGCTGAGGCTGGGCCTGGCCCACGGGCCTA 2412
          ||||||||||||||||||||||||||||||||||||:||:||:||
Db   775 SerProSerLeuSerProSerLeuSer--------ProAlaLeuAlaGlyGlnGlyHis 791
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Qy    472 GCACGATCCAAAGCGTTCAATGCCAACCGGCCGGGGGGGCCGAGGCCGTGCTCTACCACCTG 531
           |||||                                |||  ::  ||| :||||||||||||
Db    200 Ala-----------GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu 216

Qy    532 TCCGGGCACCTGCAGAAGAGCAGCCCAAGGGC---AAGCACAAGTCAATAAGGGG 582
           |||||||||   :::          :::       ||||||||
Db    217 SerGlyHisTyrLysProGlyLysGlyLysThrLysLeuGlyAsnAsn 236

Qy    583 ---GTGTTTGGGAGGAGAAACCAACTTGCCTGAGTACAAAGTAGCGCCAATCCGGAAGTCG 639
                :::|||||||||||||||||                ::||||:::::||||||
Db    237 PheMetHisSerThrGluIleAlaProPheProGluTyrLysThrGlnSerIleLysLysSer 256

Qy    640 GCCACACTCTATGTGCTGCACTGTGGGCCACTGAGCGACCCACCTTCATCCTGCTC 699
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Db    257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTyrLysLeuGlyLysSer 276

Qy    700 CCCAGTGCCGCCCGGCAGCGCCCAGCCGTCTGTGACCTGGCACGGGAGGTTCTTTCATC 759
           ::|||||||          ||||||||||     ||||||||:::
Db    277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 296

Qy    760 CCCAGTGCCGCCCGGCAGCGCCCAGCCGTCTGTGACCTGGCACGGGAGGTTCTTTCATC 819
              :::||||                       :::||||||||
Db    297 GlnThr------------LysValSerAspValIleLeuValGlnLeuAlaLeuPheIle 310

Qy    820 CTTGACATTGTGCTGAATTTCCGTACCACCATTCGTGGGCCCAGGTGTGGTGTTT 879
                                 ||||||  :::::||||||||:::
Db    311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyValValSer 330

Qy    880 GCCCCAAAGTCCATTTGCCTCACTACGTCACCACTGGTTCCTGCGTCGGGAATGTCATCGGA 939
           :::|||||||:::                         ::::|||||||||
Db    331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTrpPheAlaLeuAspLeuLeuAla 350

Qy    940 GCGCTGCCCTTGACCTGCTCACATGCCTTCAAGGTCAACGTTGTTACTTCGGG 990
                                 ||||||||||:::::
Db    351 AlaLeuProPheAsp--------HisLeuTyrAlaSerAspLeuTyrAspGlyLeuAspSer 368

Qy    991 ---GCCCATCTGCTGAAGACGGTGCGGCCTCGGCTTCCGGCCTG 1047
                   ||||||||:::||||||||||||||
Db    369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuLeuGlnLysIle 388

Qy   1048 GACCCGGTACTCCGACGTACAGCGCGTTGGTGCTGACAGTGCCATGGCCGTGTTCGCCCTG 1107
              ||||||||||:::|||||||||                 :::||||||
Db    389 AspArgArgTyrSerGlnHisThrAlaMetIleLeuGluThrLeuLeuMetPheSerPheThrLeu 408

Qy   1108 CTCGGCCACTGGGGTGCCTGCGTTGGGTTTTTACATTGGCCAGCGCGGAGTCGAGAGCAGC 1167
           :::|||||||||                        :::|||||||||
Db    409 AlaAlaHisHisTrpLeuAlaCysValIleTrpTyrValIleLeuAlaValLysGluTyrGlu 426

Qy   1168 GAATCCGAGCTGCCTGAG---ATTGGCTGGCTCGCAGGAGTCTGGCCCGCCGACTGGAG 1221
              |||||||||          |||||||||::::
Db    427 ---TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGlyArg--- 442

Qy   1222 ACTCCCTACTACCTGGTGGGCGGAGGCCAACTGAGGAACAGCTCCGGCGAGAGTGAC 1281
           :::||||||||||||||                         :::||||||
Db    443 -----LysAsnAlaSerValAlaIleLeuLeuThrThrAlaGlu--- 454

Qy   1282 AACTGCAGCAGCAGCAGCCAACGGACGGGGCTGCTGGGGGGCCGTG 1341
           :::|||||||||||||||||||               :::
Db    455 -----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerValGly 471

Qy   1342 CTGGGCACGGCCCTGACTACACTCCCTCTACTTCGGCACGAGGCTCACCAGCTGGGC 1401
           :::||||||||||||||||||                    :::|||||||
Db    472 PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrThrAlaGlu--- 491

Qy   1402 TTCGGCAACGTGTCCGACACAACGGACGAGAGATCTTCCCATCCTCCACCATGCTC 1461
           :::|||||||||||||||||||               |||||||
Db    472 PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrThrAlaIleIleMetMetLeu 491

Qy   1462 ATCGGCGGCCCTGATGCACGGGTGGTGTTTGGGGAACGTGACGACGCCATCAACCCAGCTGCATG 1521
           :::||||||||||||||                    :::|||||||
Db    492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrThrAlaIleIleGlnArgMet 511

Qy   1522 TACGGCCCCGGCTTTCTGTACCACAGCCGCACGCGCGGACCTGCGCGACTACACATCCGCATC 1581
           :::||                                 ||||||
Db    492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrThrAlaIleIleGlnArgMet 511
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Db    512 TyrSerArgArgSerLeuTyrGluSerLysLysTrpArgAspLeuLeuSerValAlaLeu 531

Qy   1582 CACCGTAATCCCCAAGCCCTCAAGCACGCCGCCATGCCACCATGCTGGAGTACTTCCAGGCTG 1641
           |||                 ::                  :::|||||||
Db    532 HisAsnAspMetProLysGluLysGlyAsnLeuArgGluAspTyrPheGlnThrSerTrpSer 551

Qy   1642 GTGAACAATGGCATTCGACGACCACCAGAGTGCTGCCAGACCTCCTGCGGCCAGCCA 1701
           :::|||||||||||||||                    ::||||||
Db    552 LeuSerIleSerGlyIleAspIleTyrGluThrLeuArgLeuPheProGluLeuArgGly 571

Qy   1702 GACATCGCCACCTGCACAAAGGAGGTTCTGCAGCTGCCACTGTTGAGGTGCAGC 1761
           :::||||||||||||||                    ::||||||
Db    572 AspValSerMetHisGlyIleLeuAspIleTyrGluThrLeuArgLeuLeuProIleLeuAlaSer 591

Qy   1762 TACCTCATTCCACCAAGGCGATGCCCTCGTCTCTGGCCTCCAGGCCCTTCTGCACGCGGGAG 1821
           :::|||||||||||||                    ::||||||
Db    592 GlnGlyCysLeuLeuLeuSerLeuGlnHisIleArgGluIleLeuGluAspLeuProIleGlu 611

Qy   1822 GAGGTGCTCAAGGGTGGCACCGTGCTGCCCATCCTAGGGAAGGGCGACACTGATCGGCTGT 1881
           :::|||||||||||||                    ::||||||
Db    612 TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysSerAspMet 631

Qy   1882 TACCTCATTCCACCAAGGCGATGCCCTCGTCTCTGGCCTCCAGGCCCTTCTGCACGCGGGAG 1941
           :::|||||||||||||                    ::||||||
Db    632 GluValIleLeuLysAspAspMetValAlaAlaIleLeuLeuGlyLysAspLeuValGlySer 651

Qy   1942 GAGCTG------------- 1947
           :::|||||||
Db    652 AspIleAsnValHisIleLeuValAlaThrSerAsnGlyValGlnMetThrAlaThrSer 671

Qy   1948 CCCGGCCGGAGCAGGTGGTAAAGGCCAAGCAGGGTGACTACTCGGTC 2007
           :::|||||||||||||                    ::||||||
Db    672 AlaGlyGlnAspValValAlaArgSerSerAspIleLeuLysAlaLysGlnGlyAspTyrCysAsp 691

Qy   2008 CTGCAGTGTCTGCAGCTGCAGTGGCCTGGCCGGCACCGACCAGGCTTTCGGCGTTACCCCGAGTTGCC 2067
           :::|||||||||||||                    ::||||||
Db    692 LeuLysCysIleLeuHisMetGlyGlyLeuProSerPheProLeuSerGluProSerIleGlu 711

Qy   2068 CCGGGCCTTCAGTCGTGTGGGCCTCCGGAGGGGGAGGCTCAGCTACTACAACCTGGGGTCGTGGGGGAGGC 2127
           :::|||||||||||||                    ::||||||
Db    712 GlnGlnPheAlaAsnAspIleGlnHisIleAspLeuPheThrCysAsnLeuArgGluGlyTyrGlu 731

Qy   2128 TCTCGCAGAGGTGGGACACCAGC 2169
           :::|||||||||||||
Db    732 AsnGlnAspSerAspIleGlyProSerPheProLeuSerIleSerAspAspGlu 751

Qy   2170 CTTATTGTCACGGTGGAG 2214
           ::||||||||||||
Db    752 AsnArgGluGluAspGluGlyLysGlyLysGlyGlyLysLysAsnGlyGly----GlyLysGlyGlyLys 769

Qy   2215 CCC---------- 2215
           ::||
Db    770 ProProSerGlyAlaSerProLeuHisSerAsnIleSerSerProLeuHisAlaThrArg 789

Qy   2251 AGCCCCGTGCTGTCCCGGCTGCCACCCTCATCCTCAGCTGCCAAGCTGCTATCCCA 2310
           :::|||||||||||||                    ::||||||
Db    790 SerProLeuLeuGlyMetGly-------- 798

Qy   2311 CGTTCGACAGCACCCGCCTTCCTCAGGGTGGCAGAGGGGAGGGGCCAGAGGCGAGGGGGGCCT 2370
           :::|||||||||||||                    ::||||||
Db    799 Arg-----AsnGlnArgLeuHisGlnArgGly 807

Qy   2371 TTGAAGGGTGAGGCTGGCCCCTGCCTGCTCCCCACGGGCCCTTAGGGCGTGCC 2430
           :::|||||||||||||                    ::||||||
Db    808 ------------------ArgSerLeuIleThrArgArg----- 814

Qy   2431 CCCATGCCATGGAATGTGCCCCCAGAAGTCATGAGCCCCAGGGTAGTAGATGGCAATGGGGCAATGAGAC 2490
           :::|||||||||||||                    ::||||||
Db    815 ------------------GluThrArgAsnLysArgHisArgThrLeuAsnAla----- 825

Qy   2491 GGCTGTGGCTCGGGACACCGCCCAAAGTTCTCTTTCCGCGCTGGGCCCCAGTGCTCGGCCCGGAATGT 2550
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Db    825
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RESULT 7
US-09-119-855-11

; Sequence 11, Application US/09119855
; Patent No. US2002009197A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;  FILE REFERENCE: mm1-055
;  CURRENT APPLICATION NUMBER: US/09/119,855
;  CURRENT FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-119-855-11

Alignment Scores:
  Pred. No.:              8.52e-87       Length:            1284
  Score:                  1901.00        Matches:           455
  Percent Similarity:     53.85%         Conservative:      146
  Percent Identity:       40.77%         Mismatches:        273
  Best Local Similarity:  31.22%         Indels:            242
  Query Match:            10             Gaps:              31
  DB:

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-11 (1-1284)
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         |||||||||||||||||||||||||||||||||||||||||||||||||||::::   :||:||
Db     1 MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy    61 CGGCTTCGACGGCACGAGTAACTTCGTGCTGGGCAACCCCAGGTGGGCGGGGTCTTC 120
         |||||||||||||||:|:::||:|||||||||||||||||||||:::
Db    21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39
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Qy   820 CTTGACAATTGTGCTGAATTCCGTACCAAATCGTGTCCAAGTCGGCCAGGTGGTGTTT 879
         ::::||:||:|||||:||:|||||||||||||||:::   |||:||:
Db   311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyLeuValSer 330

Qy   880 GCCCCAAAGTCCATTTGCCTCCACTACGTCACCACCTGGTTCCTGCTGGATGGCATCGCA 939
         |||||||||||::::|||:||||||||||||||||||||||:::
Db   331 AsnSerLysGlnIleIleAlaIleAsnTyrValThrThrPheLeuAspLeuLeuAla 350

Qy   940 GCGCTGCCCGTTGACCTGCTACATGCCTTCAAGGTCAAGCGTGACGTACTTCGGG 990
         :::   :||::||||||||||::::   :||:||
Db   351 AlaLeuProPheAsp------HisLeuTyrAlaSerAspLeuTyrAspGlyLysAspSer 368

Qy   991 ---GCCCATCTGCTGAAGACGTGCGGCCTGCGCGCGTCGGCTG 1047
         |||||||||||||||||||||:::   :|||:||
Db   369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuLeuGlnLeuLysIle 388
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(sequence alignment continues)

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Qy   1048 GACCGGTACTCGCAGTACAGCCCGGTGTTCGGCCGGTTGACACTGCTCATGGCGCGTGTTCGCCCTG 1107
          |||||||                                      ||||                |||
Db    389 AspArgTyrSerGlnHisThrArgAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu 408

Qy   1108 CTCGGCCACTGGGTCTCGGCCTCTGGTTTTACATTGGCGGAGATCAGACAGCAGC 1167
          :||||||||||||||||||||||||||||::||::||::||||||||||||||||
Db    409 AlaAlaHisTrpLeuAlaCysTyrIleTrpArgValIleAlaValLysGluTyrGlu 426

Qy   1168 GAATCCGAGCTGGCCCTGAG------ATTGGCGTGGCCCCAGGAGACTGGGCCGGACTGGGAG 1221
          ||||||                ||||||||||||||||||||||||||||||||||
Db    427 -----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGlyArg---- 442

Qy   1222 ACTCCCTACTACCTGGTGTGGGGACCAGGAGGAACAGCTGCCGGAGGAGTGAC 1281
          |||||||||||||||||||||||||||||||||||||||||||||
Db    442 ------------------------------------------------------- 442

Qy   1282 AACTGCAGCAGCAGCAGCCAACGGCGGCTGGAGCGTGCTGGGGGGCCCGTCG 1341
          :::::||::||||||||||||||||||||||||||||||||||||
Db    443 -----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu--------- 454

Qy   1342 CTGGGCCAGGCCTACATCACCTCCTCTACTTCGACTCACCAGCCTCACCAGGCTGGGGC 1401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    455 ------------------------------------------------------- 454

Qy   1402 TTCGGCAAGGTGTCGCCAACACCGGACACCGGAAGAGAATCTCTCCAATCTGCACCATGCTC 1461
          ||||                        ||||||||||||||||||||
Db    472 PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrIleIleMetMetLeu 491

Qy   1462 ATGGGGCGCCCTGATGCACCGCGGTGTGGTTTGGGAACGTGACGGCCCATCAATCCAGCGCATG 1521
          |||:|||||||||||||||||||||||||||||||||||||||||||||||
Db    492 IleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIleIleGlnArgMet 511

Qy   1522 TACGGCGCCGCGTTTCTGTACCAGCCGCACCGGGCCGACTACATCCGCAATC 1581
          ::::|||||||||||||||||||||||||||||||||||||||||
Db    512 TyrSerArgArgSerLeuThrGluSerIleTyrArgAspLeuArgAspPheValAlaLeu 531

Qy   1582 CACCGGTAICCCAAGCCCTCAAGCAATGCCATGCTGAGTACTTCCAGCCAGC 1641
          ||::||||||||||||||||||||||||||||||||||||||||||||
Db    532 HisAsnMetProLysGluLysGlnArgIleLeuAspTyrPheGlnThrSerTrpSer 551

Qy   1642 CGGGAACAATGGCATCGACACCACCGAGTCTCCTGCTACGAGCCTGCGCCCA 1701
          ::|||||||||||||||||||||||||||||||||||||||||
Db    552 LeuSerHisGlyIleLeuAspIleTyrGluThrLeuArgLeuAspSerLeuLysThrAsnPheCysAlaProGlyGlu 571

Qy   1702 GACATCCCCAATGCCACCTGCGACAAGGAGGTCGTCCACTGTGTTTGAGGGTGT 1761
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Db    572 AspValSerMetHisLeuHisArgGluIleLeuGlnLeuProIlePheGlnThrSerTrpSer 591

Qy   1762 CGGGGGCACCGTCTCTGGGCCCCGCCCGTCTTCGCCACCCCGGGAG 1821
          ::::||||||||||||||||||||||||||||||||||||||||
Db    592 GlnGlyCysLeuGlyLeuSerLeuSerIleLeuLysThrAsnPheCysAlaProGlyGlu 611

Qy   1822 TACCTCATTCACCAACGGCGATCCCTGCAGGCCTTACTTTGTCTGGCTCCCATG 1881
          |||||||||||||||||||||||||||||||||||||||||
Db    612 TyrLeuIleHisLysGlyAspLeuAsnAlaTyrIleTyrPheLeuCysAsnGlySerMet 631

Qy   1882 GAGGGTGCTCAAGGGTGGCACCGTGCTGCCATCCTAGGGAGGGCGACCTGATCGGCTGT 1941
          |||||||||||||||||||||||||||||||||||||||||||||
Db    632 GluValIleLeuLysAspAspMetValAlaValAlaArgSerSerAspIleLysAlaLeuThrThrTyrCysAsp 651

Qy   1942 GAGGTG- 1947
          :|||||
Db    652 AspIleLeuAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrAsnSer 671

Qy   1948 CCCCGGCGGAGCAGGTGTAAAGGCCAATGCACGTGAAGGGCGTGACGTACGTCGGTC 2007
          |||||||||||||||||||||||||||||||||||||||||||
Db    672 AlaGlyLysAspValValAlaArgSerSerAspIleLysAlaLeuThrThrTyrCysAsp 691

Qy   2008 CTGCAGTTGTCTGCAGCTGGCTGGGCTGCGGTCACGACAGACCTTCGCCGTGTTACCCCGAGTTTGCC 2067
          |||||||||||||||||||||||||||||||||||||||||||||
Db    692 LeuLysCysTyrIleHisMetGlyGlyLeuValGlyValLeuArgLeuArgTyrProGlyTyrGln 711

Qy   2068 CCGCGGCTTCCAGTCGTCGGCCTCCGAGGGGGAGGCTCAGCTACAACCTGGGTGCTGTGGGGGAGGC 2127
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Db    712 GlnGlnPheAlaLeuAsnAspAspLysGlnHisHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu 731
          ::::||||::

Qy   2128 TCTGCGAGGTGGACACCAGC------------------------TCCCTGAGCGGCGGCGACAATACC 2169
          ::::||||                                   ||||||||||||||||||
Db    732 AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleLeuSerGluGluGlyAspAspGlu 751

Qy   2170 CTTAAGTCACGCTGGAG------GAGAAGAGACAGATGGGGGAGGGC 2214
          |||                    |||||||||||||||
Db    752 AsnArgGluGluGlyGluGlyGlyGluLysLysGlyGluAlaGlnGlyGly----- 769

Qy   2215 CCC------------------ACGGGTCTCCCAGCCTGATGAGCCCTCC 2250
          |||                  ::::|||
Db    770 ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 789

Qy   2251 AGCCCCCTGCTGTCCCCCTCGGCCTCGCACCCTCCTCATCCTCACGAGCTGCCAAGCTGCTATCCCCA 2310
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 SerProLeuLeuGlyMetGly 798

Qy   2311 CGTCGAACAGCACCCCGGCGTCGTCTAGGTGGCAGAGGAGGCCAGGGAGGCAGGGGCT 2370
          |||                             ||||||
Db    799 Arg---------------------AsnGlnArgGlnLeuHisGlnArgGly----- 807

Qy   2371 TTGAAGGCTGAGGCTGCCCCCTTCGCTCCCCCACGGGGCCCTAGGAGGGGGCTAGGGCTGGCC 2430
          |||                    |||||||||||||||
Db    808 -----------------ArgSerLeuIleThrLeuArg----- 814

Qy   2431 CCCATGCCATGGAAATGTGCCCCCAGGGTGCCCCAGGGTAGTAGGAGCATTGAAGAC 2490
          ||                       ||||||||||||||||
Db    815 ------------------------GluThrAsnLysArgHisArgThrLeuAsnAla 825

Qy   2491 GGCTGTGGCTCGGGACCAGCCCAAGTTCTCTTTCCGGGTGGGCCGGAATGT 2550
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Db    826 SerGlyLysLysArgProSerLeuArgLeuAspSerGlnValSerThrThrLeuHisGln 846

Qy   2551 AGCAGCAGCCCCTCCCCCTGGGACCAGAGAGAGGCCCTGCTCACTGTTCCCCATGGGGCCCCT 2610
          |||||||||||||||||||||||||||||||||||||||||
Db    835 AspValAlaGlnLeuLeuSerArgAlaGluArgAlaArgAsnAlaIleLeuSerAlaLeuGlnMet--- 884

Qy   2611 GAGGCAAGGAACACAGACACACTGGACAAGCTTCGGCAGGGGGGTGACGAGTGTCAGAG 2670
          |||||||||||||||||||||||||||||||||||||||||
Db    845 -----------GluGluProGluLeuGluGlyGlu----------GlnSer 845

Qy   2671 CAGGTGCTGCAGATGCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTCGCAGCTTGTCCTG 2730
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Db    846 SerGlyLysLysArgProSerLeuArgLeuAspSerGlnValSerThrThrLeuHisGln 865

Qy   2731 GCGCCCACAGGGGAGGGTCCGTGCCCTCGGCCATCGGGAGGGGGCCGTGCCCAGCCAGC 2790
          :::|||||||||||||||||||||||||||||||||||||||
Db    866 AspValAlaGlnLeuLeuSerArgAlaGluArgAlaArgAsnAlaIleLeuSerAlaLeuGlnMet--- 884

Qy   2791 ACCTCCGGCGCTTCTGCAGCCTCTCGTGTGGACACTGGGCATCCTCCTACTGCTGCCGAG 2850
          ||||||||||||||||||||||||||||||||||||||||
Db    885 ---------------------------------------------------ThrPhe 886

Qy   2851 CCCCCCAGCTGGCTGTGTC------TTGAGTGGGACTGGATTGGGCCCACCCCGTCCGGGGCT 2904
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Db    887 ThrSerAlaAsnAlaMet---     -ThrSerHisSerSerLeuLysPhe--- 899

Qy   2905 CCTCCCCTCCATGGCGCACCCTGGGCCCTGGGGTCCCCAGGGTCTCAGAGCTCCCCCTGGCCT 2964
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Db    900 ProProAlaArgSerIleProAsnIleSerGly------ValAlaGlyThrArgArgSerGlyValA 919

Qy   2965 CGAGCCACAGCTTTCTGACCTCCCACCT------CAGACTCAGAGCCCCGCC 3012
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Qy   3013 TCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCC 3052
          ::|||||||||||||||||||||||||||||||||||::|||
Db    937 tGlnArgSerSerSerHisProProGluValAlaTrpProGlyArgAspValGlnLeuProThrSe 957

          ||||::|||::|||
Db    957 rAsnThrValAlaSerSerLysSerAlaProSerProValGluPro 970
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; Sequence 5, Application US/09119855
; Patent No. US2002009197A1
; GENERAL INFORMATION:
;   APPLICANT: Curtis, Rory A.J.
;   TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;   FILE REFERENCE: mni-055
;   CURRENT APPLICATION NUMBER: US/09/119,855
;   CURRENT FILING DATE: 1998-07-21
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   ORGANISM: Homo sapiens
;   TYPE: PRT
;   LENGTH: 542
US-09-119-855-5

Alignment Scores:
Pred. No.:          1.42e-83
Score:              1835.50
Percent Similarity: 77.64%
Best Local Similarity: 62.97%
Query Match:        30.14%
DB:                 10

US-09-965-830-1_Copy_6_3257 (1-3252) x US-09-119-855-5 (1-542)

                     Length:        542
                     Matches:       352
                     Conservative:  82
                     Mismatches:    92
                     Indels:        33
                     Gaps:          5
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Qy    1 ATGGCCGGCCAtNGCGGGGCGGCCCTCCCTGGGCGCCCTCAGACACCATCGCTACG 60
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Db    1 MetProValMetLysGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy   61 CGCTTCGACGGCGACGACAGTAACTTCGGTGCGGCCCCCAGGTGGGGCGGGGGCTCTTC 120
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Db   21 ArgPheAspGlyThrHisSerAsnPheIleLeuLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

Qy  121 CCCGTGGTCTACTGCTCTTCGTGATGGCCTTCTCCCGGGGCTGAGGTC 180
          |||::| |||||||||||||||||||::|||||| |||||::|||| |
Db   41 ProIleValTyrCysSerAspGlyPheCysGluGluLeuAlaGlyPheAlaArgThrGluVal 60

Qy  181 ATGCAGCGCGGGGCTGTGCCTGCTCCTTCCTTTATGGGGCCAGACAGCTTCCGGC 240
          ||||| |||| ||::|||||||||||||||||||||||||||||||||| |:::|
Db   61 MetGlnLysSerCysSerLysPheLeuPheGlyValGlyThrAsnGluGlnLeuMet 80

Qy  241 CAACAGAAtCCGACAAGGCCCTGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
          |||||  ||||||||||||||||||||||||||||||||||||||||||||||   |||
Db   81 LeuGlnIleLeuGlnLysSerLeuGluGlyLysThrGluPheLysGlyGluIleMetPheTyr 100

Qy  301 CGGAAGAGCGGGGCTCCCGGTTCGGTGTCTCGTCCTGGATGTGATACCCATAAAGAATGAGAA 360
          :: ||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db  101 LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120

Qy  361 GGGGAGGTGGCTCTCTTCCTTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
          |||::||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db  121 GlyAspValValLeuPheLeuLeuSerPheLysAspIleThrAspThrLysValLysIle 140

Qy  421 GGCCCCGACAGAtGGAAGGAGGAGACAGGTGTGGGCGGGCGGGCGGGCACGATCC 480
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Db  141 ThrProGluAspLysLysGluAsp--------LysValLysGlyLysAlaArgSerArgAla 156

Qy  481 ---AAAGGCTTCAATGCCAACCAGGGGGCGGGGGGAAGCCCCGTGCTCTACCACCTGTCCGG 537
          ||||||::|::||||||||||||||||||||::||||:::||||||||||||::|
Db  157 GlyThrHisPheAspSerAlaAlaArgAlaValLeuTyrHisIleSerGly 176

Qy  538 CACCTGCAGAAGCAGCCCAAGGGCACAGCTCAAtAAGGGGTGTGTTGGGGAGAAA 597
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Db  177 HisLeuGlnLysArgGlnLysGlyThrAlaGlnIleLysGlyCysValGlyGluLys 196

Qy  598 CCAAACTtGCCTGAGTACAAAAGTAGCCGCGCCATCCGGAAGTGCGCCCTTCATCCTGTTGCAC 657
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Db  197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerPheIleLeuLeuHis 216

Qy  658 TGTGGGGCACTGAGAGCCCACCTGGGAtNGGCTTCATCCTCGCCACACTCTATGTGGCT 717
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Db  217 PheSerThrPheLysAlaGlyTrpPAspTrpIleLeuLeuLeuAlaThrPheTyrValAla 236
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Qy  718 GTCACTGTGCCCTACTACGGTCGTGTTGTGTGAGCACAGACACGGAGGAGCCCAGTGCCCGCGGGC 777
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Db  237 ValThrValProTyrAsnValCysPheIleGlyAsnAspAspLeuSerThrThrArgSer 256

Qy  778 CCGCCCAGCGTGTGCAGGTCTGTTGGACCTGGCCGTGGAGGTCCCTTCATCCTTGACATTGTGGAAT 837
          |||||||||||||||||||||||||||::|||||||||||||||| ||| |||||||||
Db  257 ---ThrThrValSerAspIleAlaValCysPheIleGlyAsnAspAspLeuSerThrThrArgSer 275

Qy  838 TTCCGTACCACAtTCGTGTCCAAGTCGGGCACCAGGGAGGTCCCCAAAGTCCAtTTGC 897
          ||||| ||| |||||||||||||||||||||||||||||::||
Db  276 PheArgTyrHisThrTyrValSerLysSerGlyValValProIleGlnAlaProIleTyrAsn 295

Qy  898 CTCCACTAACGTCACCACCTGGGTTCCTGGCGTGGATGtCATCGCACGGACGGTTTGCCCCTTGACCTG 957
          ::|||||||||||||||||||||||||::||||||||::|||||||||||::||||||
Db  296 IleHisTyrValThrThrTrpPheLeuAspLeuAlaLeuAlaLeuProPheAspLeu 315

Qy  958 CTACACGTGCCTTCAAGGTGCAAACGTGTACTTCGGGGGCCCATCTGCTGTGCAAGGACGTTGGCGCCTG 1017
          |||||::||::|||||||||||||||||||||||||||||::||| |||::|||
Db  316 LeuTyrArgAlaPheAsnValThrValSerLeuVaIHisIleLeuLeuLysThrValArgLeu 335

Qy 1018 CTGGCGCCTGCTCAGCGGGGAGAGGATCGAGAGCAAGCCACGGAACCTGGAGCGTCGAGATTGGCTGGCTG 1077
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Db  336 LeuArgLeuLeuArgLeuGlnIleLysLeuAspAspArgTyrSerGlnHisSerThrIleVal 355

Qy 1078 CTGACACTGCTCAtGTGGCCGTGTTCGCCCCTGCTCGGCGCACTGGGGTGGGGTTGTTTGGGTT 1137
          |||||||::|||| ||||||||||||||::|||||||||||||||::|||||
Db  356 TACAtTGCCCAGGCGGGGAGAGATCGAGAGCATGATGCTTGTGGGCTG 375

Qy 1138 TACAtTGCCCAGGCGGGGGAGAGAtCGAGAGCATGATGCTTGTGGGCTG 1197
          |||:::|||||||||||||||||||||||||||||||||||||||::|||
Db  376 ValIleGlyValPheGluArgGluAspAsnSerLeuLeuGlyValGlyTrpLeu 395

Qy 1198 CAGGAGCTGCGCCCGCCGACTGGAGAGAGCTCCCTACTACCTGTGGGGCGGAGGCCCAGGCTGGA 1257
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Db  396 HisGluLeuGlyLysGlyLeuGluSerProTyrTyr-------- 407

Qy 1258 GGGGAACAGCTtCCGGCGCCAGAGTGACAACTGCAGCACCACGAGGCCAACGGGGGACGGGG 1317
          |||||||||| ||||||||||||||||||||||||||||||||||||--------
Db  408 GlyAsnAsnThr----------- 411

Qy 1318 CTGGGAGCtGGCTGGGGGGCGCGCCCGTTCGCCGAGCGCCGCTACAttCCCTCTACTTCGCA 1377
          :::|||||||||||||||||||||||::::||||||||||::|||
Db  412 ------LeuGlyLeuProSerIleArgSerAlaTyrrIleAlaLeuAlaLeuTyrrPheThr 428

Qy 1378 CTCAGCAGCCTCACCAGCGTGGGCTTCGGCCAACGTGTCCGGCCAACACGGACGACGAGAAG 1437
          :| |||||::||||||||||::|||| |||::||::|||||||||||||||||::
Db  429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAspGluLys 448

Qy 1438 AtCTTCTCCAtTCGCACCATGTCTCATCGGCGCCCCCCCATGAtCCACGAGGTTGGTTTGGGAAC 1497
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Db  449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisSerLeuValPheGlyAsn 468

Qy 1498 GTGACGGCGCCAtCCATCCAGCAGCAtGTACGGCCGGCGTtTCGTACCCAGGCCCATGGGC 1557
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Db  469 ValThrAlaIleIleGlyIleArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488

Qy 1558 GACCTGGCGGACTACATCCGCAtCCAAGCCCTACCCAAGCCAGCGGCATGCTG 1617
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Db  489 AspLeuAlaAspTyrIleArgIleHisHisLeuProGlnLeuGlnArgMetLeu 508

Qy 1618 GAGTACTTCCAGGCCACCTGGGCGGTGAACAAtGGCAtCGACAACCACCGAGCTGCTG 1674
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Db  509 GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluValMet 527
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RESULT 9
US-10-000-151B-3
; Sequence 3, Application US/10000151B
; Publication No. US20030013136A1
; GENERAL INFORMATION:
;   APPLICANT: Balser, Jeffrey R.
;   APPLICANT: George, Alfred L.
;   TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
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FILE REFERENCE: Vanderbilt Ref No. US20030131136A1 VU0120; Attorney Docket No. US2003
CURRENT APPLICATION NUMBER: US/10/000,151B
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1

SEQ ID NO 3
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-151B-3

Alignment Scores:
Pred. No.:
Score: 1.83e-69
                            1551.00
Percent Similarity: 44.86%
Percent Identity: 33.54%
Best Local Similarity: 25.47%
Query Match: 9
DB:

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-000-151B-3 (1-1159)

Length: 1159
Matches: 424
Conservative: 143
Mismatches: 337
Indels: 360
Gaps: 38

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Db   1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg   20

Qy   61 CGCTTCGAGGGCCACGCACAGTAACTTCGTGCTGGGCCAACGCCCAGTGGCGGGGGGCTCTTC 120
           ::|||::||| |||||||||||||:||
Db   21 LysPheGluGlyHisGlnSerArgLysGlyPheIleIleLeuAlaAsnAlaArgValGluAsnCys-- 39

Qy   121 CCCCTGGTCGTCTTGCTCCTTCCTTTATGGGCACCCAGTGACCTCAGCTCGTCCGC 180
           ||||:|||:||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db   40 AlaValIleTyrCysAsnAspGlyPheCysGlyTyrSerArgAlaGluVal 59

Qy   181 ATGCAGCGCGGCGTGCCTTGCTCCTTCCTTTATGGCCACCAGTGAGCTCGTCCGC 240
           |||||||||| |||::||
Db   60 MetGlnArgProCysThrCysSerAspPheLeuHisGlyProArgThrGlnArgAlaAla 79

Qy   241 CAACAGATCCGCAAGGCCCCTGGACGAGCGAGCAGTTCAAGGCTGAGCTGATCCTGTAC 300
           ||| ||||| |||
Db   80 ArgLysAspGlySerCysPheLeuCysLeuValLeuAlaAspValProValLysAsnGluAsp 119

Qy   301 CGGAAGAGCGGGCTCCGTTCTGGTCGTCCTCGGATGTGGATACCCATAAAGAATGAGAAA 360
           ||||||||| ||| |||
Db   100 ArgLysAspGlySerCysPheLeuCysLeuValLeuAlaAspValProValLysAsnGluAsp 119

Qy   361 GGGGAGGCTGGGCTCTCTTCCTA------GTCTCTCACAAGGACATC------ 399
           ||||||||| ||| |||
Db   120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139

Qy   400 ---------AGGGAAAACCAAGAGGGGGCCCCGACAGATGG 435
           ::||| |||
Db   140 SerProAlaHisAspThrAsnHisArgGlyProProThrTrpLeuAlaProGlyArg 159

Qy   435 ------------- 435
Db   160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuLeuThrAlaArgGluSerSer 179

Qy   435 ------------- 435
Db   180 ValArgSerGlyValGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValValAlaAspValAla 199

Qy   435 ------------- 435
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Qy   435 ------------- 435
Db   219 SerGluLeuThrProAlaProSerSerLeuAlaLeuAspGluValThrArgAlaMetA 219

Qy   435 ------------- 435
Db   239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258

Qy   576 ------------- 576
Db   259 AspAlaSerGlySerSerCysSerSerLeuAlaAlaArgThrArgSerArgGluSerCysAlaSer 278

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Db   279 ValArgArgAlaSerSerAlaAspAspProIleGluAlaMetArgAlaGlyValValLeuProPro 298

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Db   299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318

Qy   603 ------------- 603
Db   319 ThrSerAspSerAspLeuValAlaArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338

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Db   359 IleAlaProLysIleLysLysGlyValThrGluLysLysThrGlnValThrGlnValLeu 378

Qy   603 ------------- 603
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Qy   706 CTCTAIGTGGCTGACTGTGCCCTACAGCGGTGTGTGTG------------- 705
           ::||||||
Db   419 IleLeuTyrThrAlaValPheThrProTyrSerArgAlaLeuAlaPheLeuLeuLeuLeuGluGlu 438

Qy   757 GAGCCCAGTGCC------------- 801
           ||| |||
Db   439 GlyProProAlaThrGluCysGlyTyrValAlaCysGlnProLeuAlaValAlaAspLeuIle 458

Qy   802 GTGGAGGTCCTCTTCATCCTTGACAITGTGCTGGAATTTCCGTAGCCATTGCTGTCCAAG 861
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Db   459 ValAspSerIleMetPheLeuGluLeuIleLeuAsnPheArgThrThrTyrValAlaAsnAla 478

Qy   862 TCGGGCCCAGGTGGTGTTTTGCCCCAAAGTCCATTGGCTCCCACTACGTTCACCACCTGGTTC 921
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Db   479 AsnGluGluValValSerHisSerProGlyArgIleLeuAlaValHisSerTyrPheLysGlyTrpPhe 498

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Db   499 LeuLeuAspSerMetValAlaLaiLaiAlaIleProProPheAspLeuLeuLeu 511

Qy   982 TACTTCGGGCGCC------------- 1023
           |||
Db   512 IleProGlyLysSerGluLeuGlyLeuLeuLysThrAlaArgLeuLeuArg 531

Qy   1024 CTGCTGCCCTGCCTGTTCCCGGCGTTGGACCCGGTACTACGCCGAGATTGGCTGCAGGAG 1083
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Db   532 LeuValArgValAlaLaiArgGlyLeuAspArgAspArgThrSerGlyGluTrpLeuHisAsn 551

Qy   1084 CTGCTCATGGCCCGTGTTCGGCCCTGCTCCCGGCCCACTGGGGTGCGGCTCGTGTTTTTACATT 1143
           |||||||||||||
Db   552 LeuLeuMetCysThrPheAlaLeuHisTrpLeuValAlaLeuAlaHisTrpLeuAlaCysIleLeuTrpIleProTyrValAlaIle 571

Qy   1144 GGCGAGCGGGAGATCGAGCAGCAGAATCCGAGCCTGCCTGAGATTGGCTGCAGGAG 1203
           ||| ::||||||
Db   572 GlyAsnMetGluGlnProHisMetAspSer------ArgIleGlyTrpLeuHisAsn 588

Qy   1204 CTGGCCCGGCCCGACTGGAGACTCCCTACTACCTGGTCGCCGGAACCCAGAGGAAC 1263
           ||||||| ::||||||
Db   589 LeuGlyAspGlnIleGluGlyLysProTyr-------Asn 598

Qy   1264 AGCTCCGGCCAGAGTGGACAACTGCAGCAGCAGCAGGCCAACGGACGGGGGGCTGGAG 1323

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              |||||||||
Db        599 SerSerGly--------------------------------------------------- 601

Qy       1324 CTGCTGGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGC 1383
                 |||||||||||||||::::::      |||:::|||:::|||||||||      |||
Db        602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620

Qy       1384 AGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATCTTC 1443
              |||||||||||||||||||||||||||||||||   ||||||::::::||||||||||||
Db        621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640

Qy       1444 TCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTGACG 1503
              |||||||||   ||||||||||||:::||||||:::|||   :::||||||||||||:::
Db        641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660

Qy       1504 GCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCACAGCCGCACGCGCGACCTG 1563
              |||||||||||||||:::|||:::            ||||||::::::         :::
Db        661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680

Qy       1564 CGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCGCATGCTGGAGTAC 1623
              |||::::::||||||   |||:::||||||   ||||||:::||||||:::   ||||||
Db        681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 700

Qy       1624 TTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGCCTC 1683
              ||||||      |||:::      ||||||||||||         :::|||:::
Db        701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720

Qy       1684 CCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTGCAG---CTG 1740
              |||:::   |||:::|||||||||   :::||||||::::::   :::||||||
Db        721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 740

Qy       1741 CCACTGTTTGAGGCGGCCAGCCGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCCC 1800
                    |||      |||::::::||||||||||||||||||::::::      :::
Db        741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760

Qy       1801 GCCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860
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Db        761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780

Qy       1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGCTCGCCATCCTAGGG 1920
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Db        781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValValAlaIleLeuGly 800

Qy       1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980
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Db        801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820

Qy       1981 GACGTGAAGGGGCTGACGTACTGCGTCCTGCAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2040
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Db        821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 840

Qy       2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCCGCGCTTCAGTCGTGGCCTCCGAGGGGAGCTC 2100
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Db        841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu------GluIle 858

Qy       2101 AGCTACAACCTG------------------GGTGCTGGGGGAGGCTCTGCAGAGGTGGAC 2142
              ::::::||||||                              ||||||   |||::::::
Db        859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878

Qy       2143 ACCAGCTCCCTGAGCGGCGACAATACCCTTATGTCCACGCTGGAGGAGAAGGAGACAGAT 2202
                                            :::|||               :::   |||
Db        879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898

Qy       2203 GGGGAGCAGGGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTG 2262
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Qy       2263 TCCCCTGGCTGCACCTCCTCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCA 2322
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Db        902 ---ProGlyGluValSerAla------------------LeuGlyProGlyArgAlaGly 914

Qy       2323 CCCCGGCCTCGTCTAGGTGGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAG 2382
                    |||            |||||||||||||||
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Db        915 AlaGlyPro------SerSerArgGlyArgProGlyGlyProTrpGlyGluSerProSer 932

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Db        933 SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSerPro 952

Qy       2419 CTACGGCTG------------CCCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCC 2466
              |||||||||               |||   |||         ||||||         |||
Db        953 LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGlyGluPro 972

Qy       2467 AGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCAAG------------ 2514
                 :::::::::      |||            :::      |||
Db        973 ---LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991

Qy       2515 ------------------TTCTCTTTC------------------CGCGTGGGCCAGTCT 2538
                                |||||||||                  |||      |||
Db        992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1011

Qy       2539 GGCCCGGAATGTAGCAGCAGCCCCTCCCCTGGACCAGAGAGCGGCCTGCTCACTGTT--- 2595
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Db       1012 LeuProArgCys---------------ProAlaProThrProSerLeuLeuAsnIlePro 1026

Qy       2596 ---------------------CCCCATGGGCCCAGCGAGGCAAGGAACACAGACACACTG 2634
                                   |||   |||      |||:::|||            |||
Db       1027 LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg------------Leu 1042

Qy       2635 GACAAGCTTCGGCAGGCGGTGACAGAGCTGTCAGAGCAGGTG---CTGCAGATGCGGGAA 2691
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Qy       2812 CTGTGTGTGGACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTG 2871
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Db       1081 ----ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099

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Qy       2932 GGTCCCCAGCGTCTC----------AGAGCTCCCCTGGCCTCGAGCCACAGCTTTCTGG 2982
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Db       1111 -ValSerGlnPheMetAlaCysGluGluLeuProProGly---AlaProGluLeuProGl 1129

Qy       2983 ACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCAGCACC 3042
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Db       1129 nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149

Qy       3043 CCTG 3046
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RESULT 10
US-10-193-692-5
; Sequence 5, Application US/10193692
; Publication No. US20030074682A1
; GENERAL INFORMATION:
;  APPLICANT: Exelixis Deutschland GmbH
;  TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF A NOVEL TELEOST POTASS
;  FILE REFERENCE: AR02-005C
;  CURRENT APPLICATION NUMBER: US/10/193,692
;  CURRENT FILING DATE:  2002-07-11
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1159
;   TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-193-692-5

Alignment Scores:
Pred. No.:                   1.83e-69
Score:                       1551.00          Length:        1159
Percent Similarity:          44.86%           Matches:        424
Best Local Similarity:       33.54%           Conservative:   143
Query Match:                 25.47%           Mismatches:     337
DB:                          9                Indels:         360
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US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-193-692-5 (1-1159)

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Db     21 LysPheGluGlyGlnSerArgLysPheIleIleIleAlaAsnAlaAlaArgValGluAsnCys--- 39

Qy    121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGGCTTCTCCCGGGGGTGTC  180
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Db     40 AlaValIleTyrCysAsnAspGlyPheCysAspLeuCysGlyThrTyrSerArgAlaGluVal  59

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          ||| || |||||||||||||
Db     60 MetGlnArgProCysThrCysTrpTrpLeuHisLeuGlyProArgThrGlnArgArgAlaAla  79

Qy    241 CAACAGATCCCAAGCCCCTGGACGAGCACAAGGAGTTCAAGGCTGACTCTGATCCTGTAC  300
          ||||||||::||| |||||||||||||||||
Db     80 AlaGlnIleLeuGlnAlaLeuUlyLeuUlyAlaLeuUluArgLysUluIleUluAlaPheTyr  99

Qy    301 CGGAAGAGCGGGGCCTCCCCGTTCTGGGTGTCTCCTGGATGGTGAATCCATAAAAGAATAGAGAAA  360
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Db    100 ArgLysAspGlyGlyPheLeuCysSerLeuValAlaProValLysAsnGluAsp  119

Qy    361 GGGGGAGGTGGCTCTCTTCCTA-------  378
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Qy    400 --------AGCGAAACCAAGAACCAGGAGGGGGGGCCCGACAGATGG--  435
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Db    140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg  159

Qy    435 ------  435
Db    160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuUrTrhIleArgGluSerSer  179

Qy    436 ---AAGGAGACAGGTGGTGGCCGGGCCGATATGGCCGGGC---ACGATCCAAAAGCGTTC  489
          || :::::|||
Db    180 ValArgSerGlyValAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspValA  199

Qy    490 AATGCCAACGGCG---  503
          |||||
Db    199 SpLeuThrProAlaAlaProSerGluSerLeuAlaLeuAspGluValThrAlaMetA  219

Qy    504 -------GCGGAGCGGCGGGGCGCGTGCTCTA-  524
          ||||||||||||
Db    219 -------GCGGAGCGGCGGGGCGCGTGCTCTA-  524

Qy    525 --CCACCTGTCCGGGCCACCTGCAGAGACAGCAGCCCAAGGGGCAAG---CACAGCTTCAAT---  576
          || |||| |||||||||||||||           |||||||||| |::
Db    239 erProProArgSerAlaProGlyGlnGlu--ProSerProArgAlaHisSerSerLeuAsnPro  258

Qy    577 ------  577
Db    259 AspAlaSerGlySerSerCysSerSerLeuAlaArgThrArgSerArgCysAlaSer  278

Qy    594 AAGGGGGTGTTGGGGAG  594
          ||||||
Db    279 ValArgArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro  298
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Qy    595 AAACCAAAC--  603
          |||
Db    299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer  318

Qy    603 ---  603
Db    319 ThrSerAspSerAspLeuValAlaArgValThrTyrArgThrIleSerLysIleProGlnIleThrLeu  338

Qy    603 ---  603
Db    339 AsnPheValAspLeuLysGlyAspProProPheLeuAlaSerProThrSerAspArgGluIle  358

Qy    604 ------  604
Db    359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu  378

Qy    379 SerLeuGlyAlaAspValLeuProGluGlyTyrGlyLeuGlnAlaProArgGlyLeuAsnSer  398
          ||||                            TTGGCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTC  645
Db    379 SerLeuGlyAlaAspValLeuProGluGlyTyrGlyLeuGlnAlaProArgGlyLeuAsnSer  398

Qy    646 ATCCTGTTGCACTGTGGGGCGCTGAGAGCCACCTGGGATGGCTTCACCCTGCTCGGCCACA  705
          ||| |||||||||||||
Db    399 ThrIleLeuLeuHisTyrSerProPheLysAlaValThrTrpAspTrpLeuLeuLeuLeuVal  418

Qy    706 CTCTATCGTGGCGTTGCCTGCGTGCCCTACGACGGTGTGTGTG------  756
          :::|||||||
Db    419 IleTyrThrAlaValPheThrProProTyrSerAlaLeuLeuLysGluThrGluGlu  438

Qy    757 GAGCCCAGTGCC----------  757                     -GCCGGCGGCGGCCCAGGTGTCTGTGACCTGGCC  801
          |||                                            ||| |::
Db    439 GlyProProAlaThrGlyLeuCysGlyTyrTyrAlaCysGlnProLeuAlaValAspLeuIle  458

Qy    802 GTGGAGGTCCTCTTCCATCCTTGACATTGTGCTGAATTTCCGTACACATTCGTTGCCAAG  861
          |||||||||| |||| |||
Db    459 ValAspIleMetPheIleValAspIlePheLeuIleLeuAsnPheArgThrThrTyrValLeuAsnAla  478

Qy    862 TCGGGCCAGGTGGTGTTTGCCCCAAAAGTCCATTTGCCCACTACGTCACCACCTGGGTTC  921
          :::                      |||||||||||
Db    479 AsnGluGluValValSerHisProGlyArgIleLeuAlaValHisTyrPheLysGlyTrpPhe  498

Qy    922 CTGCTGGATGTCATCGGAGCGTGCCCTTTGACCGTGCTACATGCCCTTCAAGGTCAACGTG  981
          |:|:|||||||||||||||||||||||
Db    499 LeuLeuAspMetValAlaAlaAlaIleProPheAspLeuLeu-----  511

Qy    982 TACTTCGGGGCC-----------  982                    CATCTGCTGAAGACGGTGTGCGCCTGCTCGC  1023
          :::                                            |||||||||||||
Db    512 IleProPheGlySerGlySerGlyGluLeuLeuIleLeuGlyLeuLysThrLeuArgGluLeuArg  531

Qy   1024 CTGCTCCCGCTGCTTCCGGGCCGCTGGACGGCGTACTCGGCAGCTACAGCCGCTGGCTGCACA  1083
          |||||||||||||||| ||:
Db    532 LeuValLeuArgValAlaAlaLysLysValLeuAspArgTyrSerGluTyrGlyLeuAlaAlaValLeuPhe  551

Qy   1084 CTGCTCATGGCCGTGTTCGCCCTCTGGTTGCGGGTCGCCTGCGGTTCGGTTGGTTTTACATT  1143
          ||||||||||                |||||| |||||||
Db    552 LeuLeuMetCysThrValPheAlaLeuTrpLeuArgValAlaCysIleTrpLeuArgValAlaIle  571

Qy   1144 GGCCAGCGGGGAGATCGAGAGCAGCGAAATCCGAGCGTGCCTGAGATTGGCGTGCTGCAGGAG  1203
          |||||||||||||||
Db    572 GlyAsnMetGluGlnProHisMetAspSer------ArgIleGlyTyrProLeuHisAsn  588

Qy   1204 CTGGCCGCGGGCCGACTGGAGACTCCCTACTACCTGGTGGCCGGAGGCAGCCACCTGGAGGGAAC  1263
          ::||||||||||| |||||
Db    589 LeuGlyAspGluIleGlyLysProTyr--  598

Qy   1264 AGCTCCGCGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACGGGGACGGGGCCTGGAG  1323
          ||||||||
Db    599 SerSerGly-----  599

Qy   1324 CTGCTGGGGCGGCCCGCTGCCTGGGCAGGGCCTACATCACCTCCTCTACTTCGGCACTCAGC  1383
          ||||||||||||||||:::::
Db    602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer  620

Qy   1384 AGCCTCACCAGCGGTGGCTTCGGCAACGTGTCCGCCAACACGGACGACCGAGAGAGTCTTC  1443
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Qy   621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640
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Db  1444 TCCATCCTGCCACCATGCTCATCGGGTTTGGGAACGTGAGCCCTAATACGAACAGCGAGAAGATTTTC 1503

Qy   641 SerIleCysValMetLeuIleGlySerLeuMetPheTyrAlaSerLeuProAsnValSer 660
Db  1504 GCCATCATCCAGCGGCCATGTACGCCCGGCTTCTGTACCAGAGCCCAGCACCGGAACCTG 1563

Qy   661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
Db  1564 CGCGACTACATCCGGCCATCCCAAGCCCGTATCCCACGCACCGATGCTGCTGGAGTACGTG 1623

Qy   681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 700
Db  1624 TTCCAGGCCACCTGGGCGGTTGAACAATGGCATGACAACACCGAGCTGCTGCAGAGCCCTC 1683

Qy   701 PheGlnHisAlaTrpSerThrTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720
Db  1684 CCTGAGCAGCTGCGGGCCAGAGACATCCCACGCACCGCTGGTGGTTTGGGGAGTGGAGTAC 1740

Qy   721 ProGluCysLeuGlnHisAlaAspIleCysLysHisLeuAsnArgSerLeuLeuGluHisCys 740
Db  1741 CCACTGTTTGAGGCGGCTGATCGGCCACCGGCCCGAGTACGTCTCTCTTGCGCGCC 1800

Qy   741 LysProHisAlaGlyAlaThrIleArgLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760
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Qy   761 ThrHisAlaProProGlyAspThrLeuValHisSerAlaGlyAspLeuLeuThrAlaLeuTyr 780
Db  1861 TTTGTGCTGCTTGGCTCCATGGAGGTGCTCAAGGTGGTCAAGGTGGTTTCAGGTTATCAGG 1920

Qy   781 PheIleSerArgGlySerIleGluIleLeuLeuArgGlyAspValValValAlaIleLeuGly 800
Db  1921 AAGGGGCGACCTGATCGGCTGTGCTGCCGGGGCGGGTGGTGGTTGTAAAGGCCAATGCC 1980

Qy   801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820
Db  1981 GACGTGAAGGGGCGTACAGGTGCTCAGGGCTGCGCCATCCTAGGCCGTGGCCTGCCGAC 2040

Qy   821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 840
Db  2041 AGCCTTGCGGTGTACCCGGAGTTTGCCCGGCCTTGCCTTCAGTCGTGTGGCCTCCAGGGGAGGCTC 2100

Qy   841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu------GluIle 858
Db  2101 AGCTACAACCTG------GGTGCTGGGGAGGGGCTCTGACAGGTGGAC------GluIle 2142

Qy   859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlyThrThrGluLeuGlu 878
Db  2143 ACCAGCTCCTGAGCGGCGACAATACCCTTATGTCCACGGCTGGAGAAGGAGAGAGAT 2202

Qy   879 GlyGlyPheSerArgGlnArgArgLysIleSerLeuProArgArgThrAspArgAsp 898
Db  2203 GGGGAGCAGGGCCCACGGTGTCCCCAGCTGATGAGCCCTCCAGCCCCTGCTG 2262

Qy   899 ThrGluGln------------GGTGCTGGG...   901
Db   841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu------GluIle 858

Qy   915 AlaGlyPro-----ProGlyLysValSerAla----- 914
Db   902 ---ProGlyValSerAla-----LeuGluLeuProGlyArgAlaGly 932

Qy   933 SerGlyProSerProGluSerGluAspGluGlyProGlyArgSerSerSerPro 952
Db   933 SerGlyProSerProGluSerGluAspGluGlyProGlyArgSerSerSerPro 952
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Db   953 LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGlyGluPro 972
Qy  2467 AGGGAGTAGATAGGCAATTGAAGACGGCTGTGGCTTCGGGAC...CAGCCCAAG------ 2514

Db   973 ---LeuMetGluAspCysGluLysSerSerAspAsnThrCysAsnProLeuSerGlyAlaPhe 991
Qy  2515 ------------TTCTCTTTC-----------CGCGTGGGGCCCAGTCT------ 2538

Db   992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1011
Qy  2539 GGCCCGGAAATGTAGCACGACAGCCCTCCCCTGCTCACTGTT--- 2595

Db  1012 LeuProArgCys------------ProAlaProThrProSerLeuLeuAsnIlePro 1026
Qy  2596 --------CCCATGGGCCCAGCGAGGCAAGGAACACAGACACTG------Leu 1042

Db  1027 LeuSerSerProGlyArgArgProArgProGlyGlyProGlyGluProGlyGlyGluPro 1042
Qy  2635 GACAAGCTTCGGCGAGGCGGTGACAGAGCTGTCAGAGCAGGTG---CTGCAGATGCGGGAA 2691

Db  1043 AspAlaLeuAlaGlnArgLeuAsnArgGlnLeuAsnArgLeuSerArgAlaAspMetAlaThr 1062
Qy  2692 GGACTGCAGTCACTTCGCCAGGCTGTGCAGGCTTGCTCTGGCGCCCACAGGGAGGGTCCG 2751

Db  1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu 1073
Qy  2752 TGCCCTCCGGCATCGGGAGGAGGGGCCGTGCCCAGCCGACACCTCCGGCGTTCTGCAGCCT 2811

Db  1074 ------------------------ValProProAlaTyrSerAla-- 1080
Qy  2812 CTGTGTGTGGACACTGGGCCAATCCTCACTGCCGTGGCCCCAGCTGCTGTCTGTCTTG 2871

Db  1081 ---ValThrThrProGlyProGlyProGly---AlaProGluLeuProGly 1099
Qy  2872 AGTGGGGACTTGGCCCCACCCTCGTCCGGGGGCCTCTCCCTCATGGCACCCTGGCCCTGG 2931

Db  1099 ----ProThrLeuThrLeuAspSerLeuSerGln 1110
Qy  2932 GGTCCCCAGGCGTCTC-------AGAGCTCCCCTCGGCTGCAGCTGGCTGCTTCTGG 2982

Db  1111 -ValSerGlnPheMetAlaCysGluGluLeuProProGly---AlaProGluLeuProGl 1129
Qy  2983 ACCTCCACCTCAGACTCAGAGCCCCCTTGCCTCCAGGAGACCTGTGCCCAGCGACACC 3042

Db  1129 nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPro 1149
Qy  3043 CCTG 3046

Db  1149 oLeu 1150
Qy  3043 CCTG 3046
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RESULT 11
US-09-735-995-2

; Sequence 2, Application US/09735995
; Patent No. US20010034024A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; TITLE OF INVENTION: SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/735,995
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/226,012
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-995-2

Alignment Scores:

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Pred. No.:
Score:                    1.83e-69
                          1551.00        Length:           1159
Percent Similarity:       44.868         Matches:          424
Best Local Similarity:    33.548         Conservative:     143
Query Match:              25.478         Mismatches:       337
DB:                       10             Indels:           360
                                         Gaps:             38

US-09-965-830-1_copy_6_3257 (1-3252) x US-09-735-995-2 (1-1159)
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Qy       1 ATGCCGCCATGGGGGGGGCCTTCCTCGGCGCCGCCTCAGAACCACTTCCTGGACAACTCGGCTACG 60
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Qy      61 CGCTTCGAGGGCACGGCACTAACTTCGTGCTGGGCACAAGTGGCGGGGCCTCTTC 120
           ::|||||||:|||
Db      21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39

Qy     121 CCCGTGGTCTACTGCTCTGATGGGTTCTTCTGTGACCTCACGGGCTTCTCCCGGGGCTGAGGTC 180
           |||::|:::|||||:||||||||
Db      40 AlaValIleTyrCysSerAsnSpGlyPhePheCysGlyTyrSerArgAlaGluVal 59

Qy     181 ATGGAGCGGGGGTTGCCGTGCCCTCCTTCCTTATGGGCCAGAACCAGTGAGCTCCGTCCGC 240
           |||||||:|||:||||||||
Db      60 ArgLysAspGlySerCysSerPheLeuCysGlyTyrSerArgAlaGluVal 59

Qy     241 CAACAGATCCGCAAGGCCCTGGGACGGACAGCAAAGGAGTGCAAGGTCTGAGCTGATCCTGTAC 300
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Db      80 AlaGlnIleLeuAlaGlnAlaLeuLeuGlyLysLysValGluIleLeuAlaPheTyr 99

Qy     301 CGGAAGAACGGGGGTCCCGGTTCCGGTGTCCCGGATGTGAATACCCATAAAGAAATGAGAAA 360
           |||||||:||||
Db     100 ArgLysAspGlySerCysSerPheLeuCysGlyTyrSerValLeuProValLeuSerAsnGluAsp 119

Qy     361 GGGGAGGTGGCGCTCTCTTCCTA------------GTCTCTCACAAGGACATC------- 399
           |||     |||                         ||||||||:::
Db     120 GlyAlaValIleMetPheLeuLeuAsnPheGluValValMetGluLeuGlyLysAspMetValGly 139

Qy     400 ---------AGGGAAACCAAGAACCGAGGGGGGGGCCCGACAGATGG----- 435
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Db     140 SerProAlaHisAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159

Qy     435 GGGGAGGTGGCGCTCTCTTCTA----- 435
           |||
Db     160 AlaLysThrProHisPheArgLeuGlyLeuProAlaLeuLeuthrThrAlaArgGlySerSer 179

Qy     436 --AAGGAGACAGGTGGTGGCCGCGGCCGGATATGGCGCCGGGC---ACGATCCAAAGGCTTC 489
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Db     180 ValArgSerGlyValAlaGlyVal-GlyAlaGlyValAla-ProGlyAlaValValAspValAla 199

Qy     490 AATGCCAACCGGGCG------------------- 503
Db     199 SpLeuThrProAlaAlaProSerSerGlyGluSerLeuAlaLeuAspGlyValThrAlaMeta 219

Qy     504 -------------------------CCGGACGCGGCGCGGCTGCTCTA--------- 524
Db     219 SpAsnHisLeuAlaLaGlyLeuGlyLeuProAlaLeuArgArgAlaLeuValGlyLeuProGlyLys 239

Qy     525 -CCACCTGTCCGGCACCTGCAGAAGGCAGCCCAAGGGCAAG--CACAAGCTCAAT--- 576
           ||||||
Db     239 erProProArgSerAlaProGlyLeuProSerProArgAlaHisSerLeuAsnPro 258

Qy     576 ------------ 576
Db     259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278

Qy     577 --------------------------AAGGGGGGTGTTTTGGGGGAG 594
Db     279 ValArgArgAlaSerSerAlaAspAspLeuGluAlaMetArgAlaGlyValLeuProPro 298

Qy     595 AAACCAAAC--- 603
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Db     299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
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Qy     603 ------------------------------------------------- 603
Db     339 AsnPheValAspLeuHisLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358

Qy     603 ------------------------------------------------- 603
Db     319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerPheArgLysIleProGlnIleThrLeu 338

Qy     604 ------------------------------------------------- 645
Db     359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378

Qy     603 ------------------------------------------------- 603
Db     379 SerLeuGlyAlaAspValLeuProGluTyrLysGlnLeuAlaProArgIleHisArgTyr 398

Qy     646 ATCCTGTTGCACTGTGTGGGGCACTGAGAGCCCACCTGGGATGGCTTCATCCCGGAGTGG 705
Db     399 ThrIleLeuHisTyrSerProPheLysSerAlaValTrpAspThrTrpLeuIleLeuLeuLeuVal 418

Qy     706 CTCTATGTGGCGTGTCACGTGTGCCCTACACCAAGCGTGTGTGTG------ 756
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Db     419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLeuGluThrGluGlu 438

Qy     757 GAGCCCAGTGCC-------------------------GCCCGCCGGCCCCAGTCGTCGTGGAACCTGGCC 801
           |||:|||                              |||
Db     439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuProLeuAlaValAlaAspIleIle 458

Qy     802 GTGGAGGTGCCTCTTCATCCTTGACATGTGCTGCGAAATTCCGTACCACATTCGTTGTGTCCAAG 861
Db     459 ValAspPheIleMetPheLeuValAlaAspLeuProPheAspArgThrThrArgThrValValAsnAla 478

Qy     862 TCGGGCGCAGGTGGGTGGTGTTGCCCCAAAGTCCCATTTGCTCCCACTACGTCACCACCTGGTTC 921
           |||||||::                                |||||||||
Db     479 AsnGluGluValValSerHisProGlyArgIleAlaValAlaHisSerTyrPheLysGlyTyrPhe 498

Qy     922 CTGCTGGAAGTGCATCGGAGCGCGCCGCCCTTGACCTGCTTACAGCCTTCAACGTG 981
           |||||||||||:||||::||||||||||||:
Db     499 LeuIleLeuAspMetValAlaAlaIleProPheAspLeuLeu 511

Qy     982 TACTTCGGGCC------------------CATCTGCTGGAAGACAGCGTGCCGCCTGCTGCGCC 1023
           |||::|||
Db     512 IleProGlySerGlyLysGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531

Qy    1024 CTGGCTCGGCGCCCTTGCTCGGCGGCTGGACGCGGTGCTACGGCGACGCGGTGGTGCTGACA 1083
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Db     532 LeuValArgValAlaAsnArgLysLeuAspAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551

Qy    1084 CTGCTCCATGGCCGTGTTCGCCCTGCTCGCGCGACTGGGTGCCGGCTCCGCCTGCTTTTACATT 1143
           ||||||||||                                      :||
Db     552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleLeuTrpTyrAlaIle 571

Qy    1144 GGCCACGCGGGAGGATCCGAGAGCGAATCCGAGCTGCCTGAGATTGGCTGGGCCAGGAG 1203
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Db     572 GlyAsnMetGluGlnProHisMetAspSer-------ArgIleGlyTrpLeuHisAsn 588

Qy    1204 CTGGGCCCGCGCCGACTGGAGACTCCCTACTACCTGGGTGGGCCGAGCGCTGGAGGGAAC 1263
           |||||
Db     589 LeuGlyAspGlnIleGlyLysGlyProTyr------------------------------Asn 598

Qy    1264 AGCTCCGGCCCAGAGTGACAACTGCAGCAGCACGCAGCCACAAGGGACGGGGGCTGGAG 1323
           ||||||||||||
Db     599 SerSerGly-------- 601

Qy    1324 CTGCTGGGCGGCGGCCCTTGCGCTGCGCCAGCCCGCTTACACTACCTTCGCCACTCAGC 1383
           |||||||||||||:::
Db     602 ---LeuGlyLeuProSerIleLeuLysSerAspLysTyrValThrArgLeuThrTyrPheThrPheSer 620

Qy    1384 AGCCTCACCAGCGTGGGCTTCGGCCAACGTGTCCGCCAACACGGACACGAGAAGATCTTC 1443
           |||||||||||||||:::||||
Db     621 SerLeuThrThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640

Qy    1444 TCCATCTGCACCATGGTCATCGGGCGCCCTGATGCACGCGGGTGTGTTTGGGAACGTGACG 1503
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Db  641  SerIleCysValMetLeuIleGlySerLeuMetThrTyrAlaSerIlePheGlyAsnValSer  660
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Qy 1504  GCCATCANCCAGTGACGCCATGTACCGCCCGCCGCTTTCTGTGACCACAGCCGCGACCTG   1563

Db  661  AlaIleIleIleAsnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal  680
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Qy 1564  CGGGACTACATCCGCACCATCCCATCCCAAGCCGTCAAGCAGCGGCCATGGGAGTAC     1623

Db  681  ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr    700
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Qy 1624  TCCCAGCCCACCTGGGGACCCGGTGAACACCCTCTGCACAGCCTC   1683

Db  701  PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe    720
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Qy 1684  CCTGACGAGCTGCGCGCAGAGCATGCCACCTTCGCACACGAGGGTCCTGCAG---CTG    1740

Db  721  ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys    740
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Qy 1741  CCACTGTTTGAGGCGGCCAGAGCCCGGCGCCTGCCCTGGGGCACTGTCTCTGGCCCGCGGCCC  1800

Db  741  LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr    760
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Qy 1801  GCTGACGAGCTGCACGCCGGGAGCTACCTCCATCCACCAAAGGGATCCCCGAGGTCCTGCAG  1860

Db  761  ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr    780
         ||:::                                      |||||||
Qy 1861  TTTGTCTCTCTGGCCCCATGGAGGGTTTCAAGGGGACCTGGACCATCCTAGG   1920

Db  781  PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValValAlaIleLeuGly    800
         |||:::                                     |||||||
Qy 1921  AAGGGGACCTGATCGGCGTGTGAGCTGCCCCGGGGACAGGTGGTAAAGGCCAATGCC  1980

Db  801  LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly    820
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Qy 1981  GACGTGAAGGGCGTGACGTACTGCGCCTCCAGTGTCTCCGACGTGCTGGGCCGACGAC  2040

Db  821  AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu    840
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Qy 2041  AGCCTTGGGCGTTGTACCCGGCTTCAGTCGTCGTGGCCGAGGGACTC   2100

Db  841  ValLeuAspMetTyrProGlyPheSerAspSerPheSerArgLeu-----GluIle      858
         |||                                        |||:::
Qy 2101  AGTCACAACCTG------------GGTGCTGGGGAGGCCTCTCGCAGGAGGTGGAC    2142

Db  859  ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu    878
         :::||||||||                                ||||||
Qy 2143  ACCAGCTCCCTGAGCGGCGGCGACAATACCCTTATTGTTCCACGGCTGGAGGAGACAGAT  2202

Db  879  GlyGlyPheSerArgGlnArgGlyLeuSerPheArgArgArgThrAspLysAspAsp     898
         |||||||                                    :::|||
Qy 2203  GGGGAGCAGGGACCCCACGGTCTCCCCAGCCCACCCCTCCAGCCCCCTGCTG        2262

Db  899  ThrGluGln------                                              901
         |||
Qy 2263  TCCCCTGGCTGCACCTCTCATCCTCGCCAAGCTGCTATCCCACGTCCTGCGAACAGCA  2322

Db  902  ---ProGlyGluValSerAla-                                       914
         |||
Qy 2323  CCCCGCCCTCCGGTCAGGTGGCAGAGGACGGGGCTTTGAAGGCTGAG             2382

Db  915  AlaGlyPro-----SerSerArgGlyArgProGlyThrGlyProTrpProGlySerProSer 932
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Qy 2383  GCTGCCCCCTCGTGCCCCCA------------------CGGGCCCTAGAGGGG         2418

Db  933  SerGlyProSerProGluSerProArgProGlyArgSerSerPro               952
         ::::||||||||:::|||
Qy 2419  CTACGGCTG-----CCCCCATGCCATGGAAATGCCCCCAGATCTGAGCCTC          2466

Db  953  LeuArgLeuValProPheSerSerProArgProProGlyGlyProGlyGlu Pro        972
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Qy 2467  AGGGTAGTAGCATGCATTGAAGAGACGGCTGTGGCCTCGGACCAGCCCAAG----------  2514


Db  973  ---LeuMetGluAspCysGlyGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
         :::
Qy 2515  ------------TTCTCTTTC-------------------CGCGTGGGGCCAGTCT        2538

Db  992  SerGlyValSerAsnIlePheSerPheTrpGlyAspSerProArgGlyArgGlnTyrGlnGlu 1011
         ||||||||:::                           |||
Qy 2539  GGGCCCGGAAGTGTAGCAGCAGACGCCCTCCCCTGGACCAGAGACGGGCCGCTGCACTGTT---  2595

Db 1012  LeuProArgCys-------                                           1026
         |||:::
Qy 2596  ------------CCCCATGGGCCCACGGCCAAGGCCAAGGAACACAGAACACTG        2634

Db 1027  LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg                1042
         |||:::
Qy 2635  GACAAGCTTCGGCCAGCCGGGTGGTCAGAGCCGTCAGAGCCAGGTG---CTGCGATGGGGAA  2691

Db 1043  AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr   1062
         |||:::
Qy 2692  GGACTGGCCAGTGCACTTCGGCCAGAGCTGTGGCAGCTTGTCCTGGCGGCCCCACAGGAGGGTCCG  2751

Db 1063  ValLeuGlnLeuLeuGln-------ArgGlnMetThrLeu                      1073
         |||:::|||
Qy 2752  TGCCCTCGGGGCATCGGGGAGGGGAGGGGCCGTGCCCAGCCACCTGCCGGGTTCTGCAGCCT 2811

Db 1074  ------------ValProProAlaTyrSerAla-                            1080
         :::|||
Qy 2812  CTGTGTGTGGACACTGGGGCATCCTTCTACTTGCCCAGCCGCCCCCCCAGCTGGCTGTCTTG 2871

Db 1081  ----ValThrThrProGlyProGlyThrSerThrSerProLeuLeuProValSerPro   1099
         |||||||
Qy 2872  AGTGGGAGCTGGCCCCACCTCGTCCGGGGGCCCCTCATGGCCACCCTGGCCCTGG      2931

Db 1100  ProThrLeuThrLeuAspSerArgGln-                                 1110
         |||:::
Qy 2932  GGTCCCCAGGGTCTC----------AGAGCTGGGCCTGCGAGGCCACAGCTTTCTGG    2982

Db 1111  -ValSerGlnPheMetAlaCysGluGlnLeuProGly-ValProProLeuProGl      1129
         |||||||:::||
Qy 2983  ACCTCCACCTCAGACTCAGAGCCCCCCTGCCCTCAGGAGAGACCTCTGCTCGTCGCCCAGCACC  3042

Db 1129  nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr    1149
         :::
Qy 3043  GGTCCCCCAGGCTCTC------                                       3046

Db 1149  oLeu 1150
         |||
Db 1149  oLeu 1150
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RESULT 12
US-09-735-995-4
Sequence 4, Application US/09735995
Patent No. US2001003402A1
GENERAL INFORMATION:
 APPLICANT: Keating, Mark T.
 APPLICANT: Splawski, Igor
 TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
 TITLE OF INVENTION: SYNDROME GENE
 FILE REFERENCE: 2323-136
 CURRENT APPLICATION NUMBER: US/09/735,995
 CURRENT FILING DATE: 2000-12-14
 PRIOR APPLICATION NUMBER: 09/226,012
 PRIOR FILING DATE: 1999-01-06
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 1159
 TYPE: PRT
 ORGANISM: Homo sapiens
US-09-735-995-4

Alignment Scores:
Pred. No.:   1.83e-69
Score: 1551.00
Percent Similarity: 44.868   Length: 1159
Best Local Similarity: 33.54%   Matches: 424
                                        Conservative: 143
                                        Mismatches: 337

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Query Match: 25.47%   Indels: 360
DB: 10   Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-735-995-4 (1-1159)

Qy   1 ATGCCGGCCATGCGGGGCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
           |||||| |||||| :::||||||||||||||||||||||||||||||
Db   1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20

Qy   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC 120
           :::|||:::||| |||:::::: ||||||:::|||
Db   21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39

Qy   121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180
              |||:::||||||:::||||||||||||:::||| |||:::|||||||||||||||
Db   40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59

Qy   181 ATGCAGCGGGGCTGTGCCTGCTCCTTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC 240
           ||||||||| ||| ||| ||||||:::|||||| |||
Db   60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79

Qy   241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
              |||||| :::|||||| :::||| ||| |||::: |||
Db   80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99

Qy   301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360
           |||||| ||| ||| ||||||:::||||||:::|||:::|||||||||
Db   100 ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp 119

Qy   361 GGGGAGGTGGCTCTCTTCCTA---------------GTCTCTCACAAGGACATC------ 399
           ||| ||| :::|||::: ||| ||||||:::
Db   120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139

Qy   400 ---------AGCGAAACCAAGAACCGAGGGGGCCCCGACAGATGG--------------- 435
                       :::||| :::|||||| ||| |||
Db   140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159

Qy   435 -- 435

Db   160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179

Qy   436 ---AAGGAGACAGGTGGTGGCCGGCGCCGATATGGCCGGGC---ACGATCCAAAGGCTTC 489
              ::: ||| ||| |||||| |||||| :::   :::
Db   180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValValAspValA 199

Qy   490 AATGCCAACCGGCG-- 503
                   ||||||
Db   199 spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetA 219

Qy   504 --------------------------GCGGAGCCGGGCCGTGCTCTA------------- 524
                                     |||||| |||||||||
Db   219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlyS 239

Qy   525 --CCACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGGCAAG---CACAAGCTCAAT--- 576
             |||||| |||||| ::: ||| ::: ||| ||||||
Db   239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258

Qy   576 -- 576

Db   259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278

Qy   577 --AAGGGGGTGTTTGGGGAG 594
                                                    ||||||
Db   279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298

Qy   595 AAACCAAAC--- 603
              |||
Db   299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318

Qy   603 -- 603

Db   319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338

Qy   603 -- 603

Db   339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358

Qy   603 -- 603

Db   359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378

Qy   604 ------------------TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTC 645
                             |||||||||||||||::: ||| ||| :::
Db   379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398

Qy   646 ATCCTGTTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACA 705
              :::|||||| :::||| |||||| |||||||||
Db   399 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuLeuVal 418

Qy   706 CTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTG---------AGCACAGCACGG 756
           :::||| |||||| ||||||||| |||
Db   419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438

Qy   757 GAGCCCAGTGCC---------------GCCCGCGGCCCGCCCAGCGTCTGTGACCTGGCC 801
              ||| ||| ||| ||| :::||| ||||||
Db   439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeuIle 458

Qy   802 GTGGAGGTCCTCTTCATCCTTGACATTGTGCTGAATTTCCGTACCACATTCGTGTCCAAG 861
           |||:::::::::||||||:::||||||::::::|||||||||||||||:::|||:::
Db   459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 478

Qy   862 TCGGGCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTCCACTACGTCACCACCTGGTTC 921
           :::   :::|||||| ||| ||| :::|||||| ||||||
Db   479 AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 498

Qy   922 CTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTACATGCCTTCAAGGTCAACGTG 981
           |||:::|||::::::||||||:::|||||||||||||||
Db   499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu--------------------- 511

Qy   982 TACTTCGGGGCC------------------CATCTGCTGAAGACGGTGCGCCTGCTGCGC 1023
              ||||||::: |||||||||||| ||||||||||||
Db   512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531

Qy   1024 CTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTGACA 1083
           |||:::|||:::   :::|||||||||||||||:::||| ||| ||||||
Db   532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551

Qy   1084 CTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGGTCGCCTGCGTCTGGTTTTACATT 1143
           ||||||||| |||||||||:::|||||||||:::||||||:::|||::: |||
Db   552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571

Qy   1144 GGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGGAG 1203
           ||| ||| :::||| ||||||||||||
Db   572 GlyAsnMetGluGlnProHisMetAspSer---------ArgIleGlyTrpLeuHisAsn 588

Qy   1204 CTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGGAAC 1263
           ||| :::::: |||||| |||
Db   589 LeuGlyAspGlnIleGlyLysProTyr------------------------------Asn 598

Qy   1264 AGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGAG 1323
           |||||||||
Db   599 SerSerGly--- 601

Qy   1324 CTGCTGGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGC 1383
              |||||||||||||||:::::: |||:::|||:::||||||||| |||
Db   602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620

Qy   1384 AGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATCTTC 1443
           ||||||||||||||||||||||||||||||||| ||||||::::::||||||||||||
Db   621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640

Qy   1444 TCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTGACG 1503
           ||||||||| ||||||||||||:::||||||:::||| :::||||||||||||:::
Db   641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660

Qy   1504 GCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCACAGCCGCACGCGCGACCTG 1563
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RESULT 13
US-09-119-855-10
; Sequence 10, Application US/09119855
; Patent No. US2002099197A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A. J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;  FILE REFERENCE: mni-055
;  CURRENT APPLICATION NUMBER: US/09/119,855
;  CURRENT FILING DATE: 1998-07-21
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 10
;  LENGTH: 1159
;  TYPE: PRT
;  ORGANISM: Homo sapiens.
US-09-119-855-10

Alignment Scores:
 Pred. No.:
 Score:                     1.83e-69       Length:           1159
                             1151.00       Matches:          424
 Percent Similarity:          44.86%       Conservative:     143
 Best Local Similarity:       33.54%       Mismatches:       337
 Query Match:                 25.47%       Indels:           360
 DB:                             10        Gaps:             38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-10 (1-1159)
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Qy      1 ATGCCGGCCATGCGGGGGCCTCCTGGCGCCCTCAGAACACCTTCCTGGACCATCGCTACG    60
          ||||||||    |||||   ||||||||:||||||||||||||||||||||||||||||||
Db      1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg   20

Qy   2467 AGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTGGGACAGCCCAAG              2514
          ||||||||    ||    ||:||||||||||||||||||||
Db    973 ---LeuMetGluAspCysGlyLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe  991

Qy   2419 CTACGGCTG------------CCCCCATTGGCCATGGAAGTCTGCCCCAGATCTGAGCCC  2466
          ||||||||||          ||||||||||||||||||||||||||||||||||||||
Db    933 SerGlyProSerSerProGluSerGluAspGlyProValArgSerSerSerPro        952

Qy   2383 GCTGGCCCCCTCTGCTCCCCA----------CGGGGCCCTAGAGGGG               2418
          ::||||||||||||||||||                ||||||||||
Db    915 AlaGlyPro-------------SerSerArgGlyArgProGlyGlyProTrpGlySerProSer  932

Qy   2323 CCCCGGGCCTCGTCTAGGTGGCAGAGGGAGGGAGCCAGGAGCTTTGAAGGCTGAG      2382
          ||||||||||||            ||||||||||
Db    902 ---ProGlyGlyValSerAla-----LeuGlyProGlyArgGlyAla  914

Qy   2263 TCCCCTGCCTGCACCTCTCTCATCCTGCCAAGCTGCTATCCCCACGTCGAACAGCA  2322
          :::||||||||                ||||||||||
Db    899 ThrGluGln------------------SerSerArgGlyArgProGlySerProSer  932

Qy   2203 GGGGAGCAGGGCCCCACGGGTCTCCCAGCCCAGCTGATGAGCCCTCCAGCCCCCTGCTG  2262
          ||||||||||||||||||||
Db    879 GlyGlyPheSerArgGlnArgGlyArgThrAspLysAsp  898

Qy   2143 ACCAGCTCCCTGAGCGCGCGACAATACCCTTATGTCCACGCTGGAGGAAGGAGACAGAT  2202
          :::||||||||
Db    859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluGluGlu  878

Qy   2101 AGCTACAACCTG-----------------------------GGTGCTGGGGAGGCTCTGCAAGGGTGGAC  2142
          :::||||||||
Db    841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu----GluIle  858

Qy   2041 AGCCTTGCGCTGTTACCCCGAGTTTGCCCCGGCGCCTTCCAGTGTCGTCTCCGAGGGAGCTC  2100
          ||||||||||||
Db    821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspAspLeuGlu  840

Qy   1981 GACGTGAAGGGGCTGACGTACTGCTGCGTCCTGCAGTGTCTGGCCCTGGTCAAGTCGGAC  2040
          ||||||||||||
Db    801 LysAsnAspIleProGlyGluProLeuLeuTyrAlaArgProGlyLysSerAsnGly  820

Qy   1921 AAGGGCGACCTGATCGGCGTGTAGGCTGATGAGCTGTGGAGCAGGTGGTAAGGCCAAATGCC  1980
          |||||||||||
Db    781 PheIleSerArgGlySerIleGluIleLeuLeuArgGlyValAspValAlaIleLeuGly  800

Qy   1861 TTTGTCGTCTGCTCTGGGTCCCATTGGAGGTGGCACCGGTCCCATCCTAGG           1920
          ||||||||||
Db    761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuThrAlaLeuTyr  780

Qy   1801 GCCTTCTGCACGCGCGGAGTACCTACTCATCCACCAAGGGGATGCCCTGCAGCCCCTCTAC  1860
          ||||||||||
Db    741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr  760

Qy   1741 CCACTGTTTGAGGCGGCCAGCCGGGCGGCCACTGTTGCGGACGCTGTGCTCTGGGCCCCC  1800
          |||||||::||||||||||
Db    721 ProGluCysLeuHisGlnAlaAlaSerPheLeuAsnArgSerLeuLeuGlnHisCys  740

Qy   1684 CCTGACGAGCCTGGCGCGCAGACATGCCACCTGCACCAAGGAGGTCCTGCAG--CTG  1740
          ||||||||||||
Db    701 PheGlnHisIleAlaTrpSerTyrThrArgAsnGlyIleAspMetAsnAlaValLeuGlyHis  720

Qy   1624 TCCCAGGCCACCTGGGGGTTGACAAATGGCATGACACCACGCTGCTGAGAGCCTC  1683
          ||||||||||||
Db    681 ArgGluPheIleArgPheHisSerGlnIleIleProAsnProLeuArgGlnArgLeuGluTyr  700

Qy   1564 CCGGACTCACTCCGCATCCACCGTATCCCCAAGCCATCGAGTAC  1623
          ::||||||||||
Db    661 AlaIleLeuGlnAlaArgLeuThrLysTyrSerGlyThrArgAlaArgTyrHisThrGlnMetLeuArgVal  680
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Qy    61 CGCTTCGACGGGCCAGCACAGTAACTTCGTTCGTTGCGTGGGGGCCAGGTGGGGGGGGCTCTTC 120
         :::|||:::|||
Db    21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys---     39

Qy   121 CCCGTGGGTCGTACTGCTCTGAGGCGTTCGTTGTGACCTCCACGGGGCTTCCCGGGCTGAGGTC 180
         |||:::|||      |||      |||
Db    40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal     59

Qy   181 ATGCAGCGGGGGCGTTGCCGTCCTCCTTTATGGGCGCCAGACACCCAGTGAGCTCGTCCGC    240
         |||      |||
Db    60 MetGlnArgGlyCysThrCysAspPheHisLeuHisGlyProArgThrGlnArgAlaAla     79

Qy   241 CAACAGATCCGCAAGGCCCTGGACGAGCAGAGTTCAAGGCTGAGCTGATCCTGTAC         300
         ||||||      |||
Db    80 AlaGlnIleLeuAlaGlnAlaLeuLeuGluGluArgGlyGlyLeuGluIleAlaPheTyr     99

Qy   301 CGGGAAGAGGGGGTCCCCGGTTCTGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAA    360
         |||||||   |||      :::
Db   100 ArgGlyAspGlySerCysPheLeuCysLeuValProValValAlaLysAsnGluGluAsp    119

Qy   361 GGGGAGGTGGGGCGTCTCCCTA----                                    399
         |||||:::|||
Db   120 GlyAlaValIleMetPheIleLeuLeuAsnPheGluLeuValValMetValGly          139

Qy   400 ---AGGCAAACCAAGAACCGAGAGGGGGGGGGGCCCCCGACAGAGG               435
         :::||      ||
Db   140 SerProAlaHisIleAspThrHisAsnHisArgGlyProProThrSerTrpLeuAlaPro... 159

Qy   435 ----------------------GTGCTCACAAGGACATC-------                435
         :::|||
Db   160 AlaLysThrPheArgLeuLeuLysProAlaLeuLeuLeuAlaLeuThrAlaArgGluSerSer 179

Qy   436 ---AAGGAGACAGGTGGTGCCCGGCCGCCGATAATGGCCGGGC---ACGATCCAAAGGCTTC 489
         |||:::|||      ||
Db   180 ValArgSerGlyGlyAlaGlyAla-ProGlyAlaGlyValAla-AspValAla          199

Qy   490 AATGCCAACCGGCG----                                           503
         ||||||
Db   199 SerProLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMeta 219

Qy   504 ----------------GCGGAGCGCGGGCCGTGTCTA------                   524
         |||||
Db   219 SerProAlaSerGlySerSerLeuAlaLysArgThrArgSerArgGluSerCysAlaSer    239

Qy   525 -CCACCTGTCCGGGCACCTGCGAGAAGCAGCCCAAGGGCAAG---CACAAGCTCAAT---   576
         |||||      |||      :::
Db   239 erProProArgSerAlaProGlyGlnLeu-ProSerProAlaGlaHisSerLeuAsnPro   258

Qy   576 ---------------------------                                   576
         |||||
Db   259 AspAlaLaSerGlySerSerLeuAlaArgThrArgSerArgGluSerCysAlaSer       278

Qy   577 spAsnHisValAlaGlyLeuGlyLeuProAlaGluGluArgArgAlaLeuValGlyProGlyLys 594
Db   279 ------------AAGGGGGTGTTTGGGGAG                                298

Qy   595 AAACCAAAC-------                                              603
         |||||
Db   299 ProProArgProHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer  318

Qy   603 -------------                                                 603
         |||||
Db   319 ThrSerAspSerAspLeuValArgGlyThrArgThrIleSerLysIleProGlnThrLeu    338

Qy   603 -------------                                                 603
         |||||
Db   339 AsnPheValAspLeuArgLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358

Qy   603 -------------                                                 603
Db   359 IleAlaProLysLysGluLysGluArgThrHisAsnValThrHrGlnValLysValThrLeu  378
```

```
Qy   604 --------------------------TTGCGTGAGTGTACAAAAGTAGCGCCCATCCGGAAGTCGCCCCTTC 645
         |||||||
Db   379 SerLeuGlyAlaAspValLeuAspGlyLeuProGlyGluGlnIleAlaProArgIleHisArgTrp :::  398

Qy   646 ATCCTGTTGCACTGTGGGGGGCCACTGAGGCCACTGGGGGATGGCTTCAGGGATGCTTCACA     705
         |||:::|||
Db   399 ThrIleLeuHisThrSerProPheLysAlaValAlaValTrpAspTrpLeuThrLeuLeuLeuVal 418

Qy   706 CCTCTATGTGGGCGTCACTGTGCCCTACTACGGGTGTGTG------AGCACGACAGG       756
         :::|||
Db   419 IleTyrThrAlaValPheThrProTyrSerAlaGluValLysPheGluThrGluGlu    438

Qy   757 GAGCCCAGTGCC-----------------GCCCGGGGCCGGGTGCCCAGCCGTGTCGTGACCTGCC 801
         |||      |||
Db   439 GlyProProAlaThrGluCysGlySGlyTyrAlaCysGlnProLeuAlaValAlaAspLeuIle   458

Qy   802 GTGGAGGTCCTCTTCATCCTTGACATTGTGCTGAGAATTTCCGTACCCACATTCGTGCCAGCA   861
         ||||||:::||||||
Db   459 ValAspSerIleMetPheIleValAlaLeuAspAspPheLeuGluIleLeuAsnPheArgThr    478

Qy   862 TCGGGCCAGGTGGTTGTTGTTTGCCCCAAAGTCCATTTGCCCGTCCACTACGTCACCACTGGTTC 921
         :::|||
Db   479 AsnGluGluValValValSerHisProGlyArgIleLeuAlaValHisSerTyrPheGly      498

Qy   922 CTGCTGGATGTCATCCGGACGGCGCCCTTTGACCTGCTACTACATGGCCTTCTACAAGGTCAACGTG 981
         |||:::|||||||
Db   499 LeuLeuAspMetValAlaLaAlaIleProPheAspAsnLeuLeu                   511

Qy   982 TACTTCGGGGGCC----------------CATCTGCTGAAGACGGTTGGCGCCTTGCGGC   1023
         |||||
Db   512 IleGluPheGlySerGlySerGluGluLeuGlyLeuLeuLeuLeuProAspLeuLeuArg   531

Qy  1024 CTGCTGGCGCCTGCGCTTCCGCGGCGTTCCAGTACGGCCGGTACTCCGAGTACAGCGGCGTGGTGTCGACA 1083
         |||||
Db   532 LeuValAlaArgValAlaLysArgLysLeuAspAspArgArgTyrSerGluTyrGlyAlaAlaAlaLeuPhe 551

Qy  1084 CTGCTCATGCGCGTTCGCCCCCTGTGCGCCCACTGGGCGTCGCGCTCGGTTTTACATT    1143
         |||||      |||
Db   552 LeuLeuMetCysThrPheAlaLeuLeuIleAlaHisSerTrpLeuAlaCysSerTrpTyrAlaIle   571

Qy  1144 GGCCAGCGCGGAGATCGAGAGCCAGCAGAAATCCGAGCTGCCTGAGATTGGCTGGCTGCGGAG      1203
         |||||
Db   572 GlyAsnMetGluGlnProHisMetAspSer------ArgIleGlyTrpLeuHisAsn       588

Qy  1204 CTGGGCCCGCCGACTGGAGACTCCCTTACTACCTGGTGGGCGGCCCAGCTGGAGGAAC      1263
         |||||
Db   589 LeuGlyAspGlnIleIleGlyLysAspProTyr-                            598

Qy  1264 AGCTCCGGCCGCCCAGAGTGACAACTGCAGCAGCAGCCAGCGAGGGGGAGGGGCTGGAG        1323
         |||||
Db   599 SerSerGly---                                                  601

Qy  1324 CTGCGGGGGGGGCCCGGCCGTCGGTGCGGAGCCGGAGGGCCTACAGCAGCCCCTACTTCGGACTCAGC 1383
         ||||||
Db   602 ---LeuGlyGlyProSerIleLeuAspLysSerTyrValThrAlaSerIleProPheHisSer    620

Qy  1384 AGCCTCACCGAGGCGTGGGCTTCGGCGAACCTGTCCCCACGGGACACCGAGAAGGAGATCTTC     1443
         |||||
Db   621 SerLeuThrThrSerValGlyTyrGlyAsnValSerProAsnThrAsnSerGluLysIlePhe   640

Qy  1444 TCCCATCTGCACCAATGCTCATCCGGCGCCCTGCGTTGATGCGCGGCGGTGGTTTGGGACGTGACG 1503
         |||||
Db   641 SerIleCysSerValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer    660

Qy  1504 GCCATCACCCACCGCAGCGTACCGCCGCGGCTTTCTGTACCACACGCCGACGGAAGATCTG      1563
         |||||
Db   661 AlaIleLeuGlnLeuArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal    680

Qy  1564 CGGGACTACATCCGATCTCCCGATGCACGCGGTGGTGTGTTGGGACTGACG              1623
         |||||
Db   681 ArgGluProPheLeuArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr   700

Qy  1624 TTCCAGCCACACTGGGGGGGTGAACAATGGCATCGACACCACCGAGCTGCTCGCGGAGCTC    1683
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Db   701  CCTGACGAGCTGTGGCGGCCCAGAGATCGCCATGCAGACTTCCTGCAG---CTG 1740
            |||     |||::::
Qy  1684  CCTGACGAGCTGTGGCGGCCCAGAGATCGCCATGCAGACTTCCTGCAG---CTG 1740
            |||||||||||||||||| :::::::
Qy   701  PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720
            :::|||||||

Db   721  ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuGlnHisCys 740
            |||||::::
Qy  1741  CCACTGTTTGAGGCGGGCCAGCGACCGCGGGCCGCTGTCTCTGGCCGCGCCC 1800

Db   741  LysProPheArgGlyAlaThrHisLysGlyCysLeuAlaLeuAlaMetLysPheLysThr 760
            |||
Qy  1801  GCCTTCTGCACGCCGCGGCGTACCTCATCCACCAAGGGAGGGGGGATGCCCTCTAC 1860

Db   761  ThrHisAlaProProGlyAspThrLeuValHisLeuGlyAspLeuGluThrAlaLeuTyr 780
            |||  :::     :::
Qy  1861  TTTGTGTCTCTGGCTCCATGGAGGGCTTCCACCGTTCGGCCCATCCTTAGGG 1920

Db   781  PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 800
            |||||:::
Qy  1921  AAGGGCGACCTGATCGGCTGTGTGAGCTGCTGCGGGGAGCAGGTGGTAAAGGCCAATGCC 1980

Db   801  LysAsnAspIleProPheGlyLeuProLeuAsnLeuThrArgAlaArgProGlyLysSerAsnGly 820
            |||||||||||||||||||      :::
Qy  1981  GACGTGAAGGGGCTGACGTACTGCGTCCTGCAGTGTCTGCACTGCCTGCACGAC 2040

Db   821  AspValArgAlaIleLeuThrTyrCysAspLeuHisLysIleHisArgAspAspIleLeuGlu 840
            |||  :::
Qy  2041  AGCCTTCGCGTCTACCCGAGTTTGCCCGCGCTTCAGTCGTGGCCTCGGAGGGGAGGTC 2100

Db   841  ValLeuAspAlaMetThrProGluPheSerAspHisPheTrpSerSerLeu------GluIle 858
            :::|||||||||||||||||:::
Qy  2101  AGCTACAACCTG------------------------GGTGCTGGGGGAGGCTTCTGCAGAGGTGGAC 2142

Db   859  ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878
            :::::::|||||
Qy  2143  ACCAGCTCCCTGAGCGGGGACAATACCCTTAYGTCCACGCTGGTGGGTGGAGAGAGAT 2202

Db   879  GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrArgProLysAsp 898
            :::
Qy  2203  GGGGAGCAGAGGGCCCCACGGTCTCCCAGCCACTGATGAGCCCTCCAGCCCCTGCTG 2262

Db   899  ThrGluGln------------------------------------ 901
            |||||
Qy  2263  TCCCCTGGCTGCACCTCCTCCATCCTGCCAAGCTGCTATCCCACGTTGCAACAGCA 2322

Db   902  ---ProGlyLeuValSerAla--------- 914
            :::::
Qy  2323  CCCCGGCCGCTCTAGGTGTGGCGAGAGGAGGGGGCCAGGCGGCTTGAAGGCTGAG 2382

Db   915  AlaGlyPro-------SerSerArgGlyArgProGlyTrpProGlySerProSer 932
            |||||||||||
Qy  2383  GCTGGCCCCTCTGCTCCCCCA------------CGGGCCCTAGAGGGG 2418

Db   933  SerGlyProSerSerProGluSerSerGlyGlyTyrArgSerSerPro 952
            :::::::||||||||||
Qy  2419  CTACGGGCTG---------------------CCCCCATGCCAGGAAATGCCCCCAGATCTGAGCCCC 2466

Db   953  LeuArgThrLeuValProPheSerProArgProGlyLeuProProGlyGluPro 972
            |||||||||||||
Qy  2467  AGGGTAGTAGATGGCATTGAAGAGCGGCTGTGGCTCGGGGACAGCCCAAG----- 2514

Db   973  ---LeuMetGluAspCysGlyLysSerSerArgAspThrCysAsnProLeuSerGlyAlaPhe 991
            :::||||
Qy  2515  ------------------------TTTCTGTTTC--------------------------CGCGTGGGCCCAGTCT 2538

Db   992  SerGlyValSerAsnIleProPheSerPheTrpProGlyAspSerArgGlyArgGlnTyrGlnGlu 1011
            |||||||||||||
Qy  2539  GGCCCGGAANGTAGCAGCACCCCTCCCTGGGACGCGGGCCTTCCTCCACTGTTT--- 2595

Db  1012  LeuProArgCys----------------------- 1026
            :::     :::
Qy  2596  ------------------------CCCCATGGGGCCCAGCAGGAGGCGGAGAACAGACACACTG 2634
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Db  1027  LeuSerSerProGlyArgProArgGlyAspValGluSerArg---------------------Leu 1042
            |||
Qy  2635  GACAAGCTTCGGCCAGGGCGGGTGACAGAGCGGTGTCAGAGGTG---CTGCAGATGCGGGAA 2691

Db  1043  AspAlaLeuGlnArgGlnIleLeuAsnArgLeuGluThrArgLeuSerAlaAlaAspMetAlaThr 1062
            |||     :::
Qy  2692  GGACTGCAGTCACTTCGCCCAGGCGTGCTGCAGCTGTTGTCCTGGCGCCCCACAGGAGGGTCCG 2751

Db  1063  ValLeuGluGlnLeuGlnLeuGln-ArgGlnMetThrLeu------------------------ 1073
            |||
Qy  2752  TGCCCTCCGGCGCATCGGACGGAGGGGGGCCGTGCCAGCCACCTCCGGGGCGGTTCTCGACGCT 2811

Db  1074  ------------------------------------------------ValProProAlaTyrSerAla-- 1080
            :::
Qy  2812  CTGCTGTGTGGGACACTGGGGGGCCATCCTCCTACTGCCTGCCTGGCTCTCGG 2871

Db  1081  ---ValThrThrProGlyProGlyProThrPheSerProThrProLeuProValSerPr 1099
            |||||||||:::
Qy  2872  AGTGGGACTTGGCCCCCACCCCTGGTCCCGGGGCCTCCCCCCTCATGGCACCCTGGCCCTGG 2931

Db  1100  oLeu------------------------ProThrLeuThrLeuAspSerLeuSerGln---- 1110
            |||||||||
Qy  2932  GGTCCCCCCAGCCGTCTC------------AGAGCTCCCCTCGGCCTCGAGCCCACAGCTTTCTGG 2982

Db  1111  -ValSerGlnPheMetAlaCysGluGlyLeuProProGly---AlaProGluLeuProGl 1129
            |||||||||||||
Qy  2983  ACCTCCACCTTCAGACTCAGAGACCCCCCCGCCGCCTCAGGAGACCTCTGCCTCCGGGACCAGCAC 3042

Db  1129  nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
            |||::::
Qy  3043  CCTG 3046

Db  1149  oLeu 1150
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Alignment Scores:
Pred. No.:
Score: 2.06e-67
Percent Similarity: 1509.50
Best Local Similarity: 49.04%
Query Match: 34.39%
DB: 24.79%
                                      9

Length: 994
Matches: 392
Conservative: 167
Mismatches: 336
Indels: 245
Gaps: 36

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-192-440-8 (1-994)

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Qy     1  ATGCCGGGCCATGCGGGGGGCCCTCCTCGGAACACCTTCCTGGACAACCATCGCTACG 60
            ||||||    :::|||||||:::||||||||||||||
Db     1  MetProValArgArgGlyHisValAlaAlaProGlnAsnThrThrTyrLeuAspThrIleIleArg 20

Qy    61  CGCTTCGACGGCACGGCACAGTAACTTCGTTGCTGGGCAACGCGCAGGTGGCGGGGCTCTTC 120
            |||:::||||::||||||||||||||||
Db       ...
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Qy     21 LysPheGluGlyGlnSerArgLysPheLeuIleAlaAlaAsnAlaGlnMetGluAsnCys--- 39

Db    121 CCGGTGGTTCTACTGCTTCTGTGATGGCTTCTGTGACCTGACCTTTCCCGGCTGAGGTC 180
            ||||::||||||      :||||||
Qy     40 AlaIleIleTyrCysAsnAspGlyPheCysGluLeuPheGluTyrSerArgValGluVal 59

Db    181 ATGCAACGCGGGGCTGTGCCTCGTCCTCTCCTTTATGGGCGACAGACACCAGTGAGCTGCCGC 240
            |||||||
Qy     60 MetGlnGlnProCysThrCysAspPheLeuPheLeuHisGlyProAsnThrProSerSerAlaVal 79

Db    241 CAACAGATCCGCAAGGCCCTGGACAGCGAGCAGAAGAGTCAAGGCTGAGCTGGATCCTGTAC 300
            :::||||      ||||||
Qy     80 SerArgLeuAlaIleAlaLeuLeuGlyLysValAspSerIleLeuTyrTyr 99

Db    301 CGGAAGAGCGGGCGGTCCGGTTCTGGGTGTCTCCCTGGATGTGATACCCATAAAGAAATCAGAGAAA 360
            |||||||
Qy    100 ArgLysAspAlaSerSerPheArgCysLeuValLeuAspValProValLysAsnGluAsp 119

Db    361 GGGGAGGTGGCTCTCTTCTTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGA--- 417
            :::||||      |||
Qy    120 GlyAlaValIleMetPheLeuLeuAsnPheGluAsnSerLeuAlaLysCys 139

Db    417                                                                  417
Qy    140 SerSerArgSerLeuSerGlnArgLeuLeuSerGlnSerPheLeuGlySerGluGlySer 159

Db    418 CGGAAGAGCGGGCGGGTCCCGGTTCTGGGTGTCTCCCTGGATGTGAT--------- 465
            |||||||
Qy    160 HisGlyArgProGlyGlyProGly--- 175

Db    466 GGGGAGGTGGCTCTCTTCTTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAG--- 498
            |||      |||
Qy    176 ArgThrIleSerGlnIleProGlnPheThrLeuAsnPheValGluProHisLysTyrSerGlyThr 194

Db    499 CGGCGGGGGAGACGGGCGGGGCCGTG-----CTCTACCACCGTGTCCGGGCAC------CTGCAG 546
            |||
Qy    195 LysHisArgSerSerThrThrGlnLeuIleLeuIleAlaProHisLysValValGlu 214

Db    547 AAGCAGCCCAAGGGCAAGGCCAAGCCAAGTAAGGGGGTGTGTTGGGGGAGAAACCAACTG 606
            :::
Qy    215 ArgThrGlnAsnValThrGlyLysValThrGlyLnValLeuSerLeuGluGlyAspValLeu 234

Db    607 CCTGAGTACAAAGTAGCCGCCAATCCGGAAGTCGCCCTTCATCGTGTTGCACTGTGGGGCA 666
            |||
Qy    235 ProGlyTyrLysLeuGlnLnAlaProArgIleHisArgThrProThrIleTyrSerPro 254

Db    667 CTGAGAGGCCACCTGGGATGGCTTCAACCTGCTCCGCACACTCTATGTGGGCTGCACTGTG 726
            |||      |||
Qy    255 PheLysAlaValTrpAspSerTrpLeuIleLeuLeuValIleLeuTyrThrAlaValPheThr 274

Db    727 CCCTACAGCCTGTCGTGTGACACAGCAGGACCCCAGTGCGCCGCCGGC----------- 777
            |||||||
Qy    275 ProTyrSerAlaLeuAlaPheLeuLeuSerArgGlnAsnAspGluSerArgArgGlyAlaCysSer 294

Db    778 -------CGGCCAGGTCGTGACCTGCGCCTGGGAGGTTCCTCTTCAGTCCTTGAC 825
            |||
Qy    295 TyrThrCysSerSerProLeuThrValAspLeuIleLeuIleValSerLeu 314

Db    826 ATTTGTGCTGAATTTCCGTACCACCAATTCGTTCTCCAAGTCTCGGCGCGTCGTTTGCCCA 885
            :::      :::||||
Qy    315 IleValIleLeuAsnPheArgTyrTyrValAsnThrAsnAspGluValSerHisPro 334

Db    886 AAGTCCAATTTGCCTCCACTACGTCACCACCTGGTTCCTGGAGTGCACGTGTTGACCTG 945
            ||||||      |||
Qy    335 ArgArgIleAlaValHisTyrProLeuTyrTrpPheLeuLeuIleAspProMetValSerSerPro 354

Db    946 AAGTCCAATTTGCCTCCACTACGTCACCACCTGGTTCCTGGAGTGCACGTGTTGACCTGGGCC 993
            :::      |||
Qy    355 ProPheAspProLeuLeuLeuProHeArgThrGlySerAspProGluThrThrThrIleLeuIleGly--- 373

Db    994 CATCTGCTTGAAGACGGTTGCGCGCGCCTGCTTCCGGCCGCTGGGACCG 1053
            ||||||:::||||      :::||||||
Qy    374 ---LeuLeuLysThrAlaArgGlyLeuArgLeuArgValAlaArgGlyLeuArgAspAlaAlaGlyGly 392
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Qy   1054 TACTCGCAGTACACGCCGCACGGGTCGGGTGGTGCTGCTGACACTGCTCATGGCGCTG 1113
            ||||      |||||||
Db    393 TyrSerGlyThrGlyIleValAlaAlaLeuPheLeueuMetCysThrPheAlaLeuAla 412

Qy   1114 CACTGGGTCGCGCCGCGTCTGGTTTTACATTGGCCAGCGGAGAATCGAGAGCAGGAATCC 1173
            |||||||      |||
Db    413 HisTrpLeuAlaCysIleLeuTrpTyrAlaLAlaIleGlyAsnValGluArgProTyrLeuGluHis 432

Qy   1174 GAGCTGCCTGAGATTGGCGTGGCTGCGCGCTGGCCGGGGTGCCCGCCGCTGGAGACTCCCTACTAC 1233
            :::||||||||||
Db    433 ---------LysIleGlyTrpLeuAspSerLeuGlyValGlnLeu------------ 444

Qy   1234 CTGGTGCGGCCCGGAGGCCAGCTGCGGGGGAACAGCTCCGGCCAGAGTGACAACTCAGCAGC 1293
            |||      |||||||
Db    445 -----GlyLysArgTyrAsnGly------ 455

Qy   1294 AGCAGCGAGGGCCAACGGGACAGGGGGCTGAGACTGCTGCCTGGCGCGCCCCGGCGC 1353
            ||||||
Db    456 ------------GlyProSerValGlnAspLys 462

Qy   1354 TACATCACCTCCCTTCTACTTCGCACTCAGCAGCCTCACCAGCGCGGTGGGGTTCGGCAACGTG 1413
            ||:::||      |||||||
Db    463 TyrValThrAlaLeuTyrPheThrPheSerSerLeuThrSerValGlyPheGlyAsnVal 482

Qy   1414 TCCGCCAACACGGACACCGAGAGAGATCTTCCATCTGCCACCATGTCCATGGGCCGCCTTG 1473
            |||      |||||||
Db    483 SerProAsnThrAsnSerGluLysSerValPheSerIleCysValMetLeuIleGlySerLeu 502

Qy   1474 ATGCACGCGGTGGTGTTGTTGGGAAACGTGACGGCCCATCACTCCAGGCCCATGTAGGCCCGCGC 1533
            ||||||      |||
Db    503 MetTyrAlaSerIlePheGlyAsnValSerAlaIleIleGlnArgLeuTyrSerGlyThr 522

Qy   1534 TTTCTTGTTACCAGCCGCACGCCGCCCACGACCTGGCGACTACAATCCGCCATCCACCGTATCCCC 1593
            |||      |||||||
Db    523 AlaArgThrValThrLeuUYrPheThrPheSerSerLeuThrSerValGlyPheGlyAsnVal 542

Qy   1594 AAGCCCCTCAAGCAGCCGCAATGCGTGGTACTTCCAGGCCACCTGGGCGTTGAACAATGGC 1653
            ||||      |||||||
Db    543 AsnProLeuArgGlnArgArgLeuGluGlyTyrPheGlnHisIleAlaProSerThrArgAsnGly 562

Qy   1654 ATCGACACCACGGAGCTGCTGCAGAGCCTCCCTGACGAGTTGCGGCACAATCGCCATG 1713
            |||||||      :::
Db    563 IleAspMetAsnAlaValLeuLeuGlyPheProGluLeuGlnHisAlaAspIleCysSerLeu 582

Qy   1714 CACCTGCACAAGGAGGTCCTGCAG---CTGCCACTGGTTTGAGGCGGCCCAGCCGCGCGGCTGC 1770
            |||      |||||||
Db    583 HisLeuHisLysArgAlaLeuLeuGlnHisLysCysProLaPheSerGlyLysAlaGlyLysCys 602

Qy   1771 CTTCGGGGGCACTGTCTCTGGCCCCGCGCCTTCTGCGACGCGGCGAGTACTCATC 1830
            :::      |||:::
Db    603 LeuArgValAlaLeuAlaValAlaValLysPheLysThrThrAlaLeuAlaArgGlySer 622

Qy   1831 CACCAAGGCGATGCCCTGCGAGGCCCCTTCTACTTTGTCTGCTTCCAATGGAGGTGCTC 1890
            |||||||      |||
Db    623 HisLeuGlyAspValLeuSerThrLeuTyrPheIleSerArgGlySerIleGluIleLeu 642

Qy   1891 AAGGGTGGCACCGTGGTGGTAAAGGGCAAGGGGCGCGTGTGACCTG 1950
            :::      |||      |||
Db    643 ArgGlyAspAspValValLysAlaLysGlyArgValTerProValSer 662

Qy   1951 CGGCGGGGAGCAGGTGGTAGGCCAATGCGACGTGAAGGGGCTGTACTCCGTCCTG 2010
            ||||||      |||||||
Db    663 LeuHisIleAlaGlnProGlyLysSerSerAlaAspValAlaGlyAlaLeuProThrArgAspLeu 682

Qy   2011 CAGTGTGTCACACTGGGCCTGCTGCACGACAGCCTTGCGCGTGTTGACCTGAGTTTGCCCCG 2070
            :::||||||      ||||||
Db    683 HisLysIleGlyLnArgAlaAspLeuLeuValLeuAspMetTyrProProAlaPheAlaGlu 702

Qy   2071 CGCTTCAGTCGTTGCGTCCGGAGGGGAGCTCAGCTACAAACCTG-----GGTGCGGGGGA 2124
            |||      |||||||
Db    703 SerPheThrTrpSerLysLeu------GluValThrPheAsnLeuArgArgAspAlaAlaGlyGly 720
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RESULT 15
US-09-119-855-8
Sequence 8, Application US/09119855
Patent No. US2002009197A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: mn1-055
CURRENT APPLICATION NUMBER: US/09/119,855
CURRENT FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
TYPE: PRT
LENGTH: 290
ORGANISM: Homo sapiens
US-09-119-855-8

US-09-965-830-1_copy_6_3257 (1-3252) x US-09-119-855-8 (1-290)

Alignment Scores:
Pred. No.:
Score: 2.49e-66   Length: 290
Percent Similarity: 1487.00   Matches: 282
Percent Identity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 24.42%   Indels: 0
    10   Gaps: 0

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Db  201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220

Qy  661 GGGGCACTGAGAGCCACCTGGGAATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

Qy  721 ACTGTGCCCTACAGCGTGTGTGTGGAGCACACCACCGGGAGCCCAGTGCCGCCCGGGCCCG 780
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Db  241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260

Qy  781 CCCACGTCTCGTGACCTGGCCGTGGAGGTCCTCTCTTCACCTGACATTGTGCCTGAATTTC 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuLeuAspIleValLeuAsnPhe 280

Qy  841 CGTACC 846
        ||||||
Db  281 ArgThr 282
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